

STIC-Biotech/ChemLib

71427

From: Collins, Cynthia  
Sent: Friday, July 19, 2002 3:13 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search request SN 09/821839

Please search, **both** prior art and interference, for SN 09/821839:

- 1) SEQ ID NO:1
- 2) SEQ ID NO:2

Thank You,

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3/29/01  
PROV. 3/31/00

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Searcher: Point of Contact  
Phone: P. Sheppard  
Location: Telephone number (703) 308-4499  
Date Picked Up: \_\_\_\_\_  
Date Completed: 8/02/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2002, 14:21:21 ; Search time 34.23 Seconds

(without alignments)  
2921.153 Million cell updates/sec

Title: US-09-821-839-2  
Perfect score: 2952  
Sequence: 1 MKEIAMRNKRKPEPTPPAG.....RTTNDNLEPCVKSLDWLGLG 578

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: sp\_archaea:.\*  
2: sp\_bacteria:.\*  
3: sp\_fungi:.\*  
4: sp\_human:.\*  
5: sp\_invertebrate:.\*  
6: sp\_mammal:.\*  
7: sp\_mhc:.\*  
8: sp\_organelle:.\*  
9: sp\_phage:.\*  
10: sp\_plant:.\*  
11: sp\_toxent:.\*  
12: sp\_virus:.\*  
13: sp\_vertebrate:.\*  
14: sp\_unclassified:.\*  
15: sp\_virus:.\*  
16: sp\_bacteriapi:.\*  
17: sp\_archaeap:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2858	96.8	648	10	Q9LQV6
2	281.5	9.5	429	10	081794
3	263.5	8.9	429	10	Q39070
4	252	8.5	443	10	Q39071
5	251	8.5	434	10	Q9XG11
6	250	8.5	428	10	Q40337
7	249.5	8.5	444	10	Q9ZU09
8	246	8.3	458	5	015996
9	243.5	8.2	429	10	Q39068
10	243	8.2	445	5	P90681
11	242.5	8.2	452	10	Q24073
12	241	8.2	424	10	Q41731
13	239.5	8.1	429	10	Q9SHP1
14	239.5	8.1	462	5	062573
15	239	8.1	457	5	Q9NIP5
16	236.5	8.0	454	10	082717

17	235.5	8.0	484	10	Q9XG10
18	234.5	7.9	445	10	Q9FG02
19	234.5	7.9	445	10	Q39067
20	233.5	7.9	427	10	Q9CAX5
21	233	7.9	460	10	Q9LDM4
22	232.5	7.9	446	10	Q04398
23	229.5	7.8	452	10	Q9S957
24	229	7.8	452	10	Q04959
25	229	7.8	480	10	Q9XG15
26	228.5	7.7	420	10	Q8S875
27	228	7.7	475	10	Q9XG14
28	227.5	7.7	454	10	Q9FVX0
29	227	7.7	456	10	Q41732
30	225	7.6	459	10	Q82718
31	223	7.5	502	10	Q43693
32	222.5	7.5	418	10	Q9SFW6
33	222	7.5	473	10	Q40516
34	220.5	7.5	378	10	Q9XG13
35	219.5	7.4	324	5	Q97478
36	219.5	7.4	470	10	Q9LQ64
37	219.5	7.4	460	10	Q941M7
38	219.5	7.4	483	10	Q04090
39	219	7.4	388	5	Q94739
40	218.5	7.4	483	10	Q40514
41	216.5	7.3	394	13	Q98SK7
42	216	7.3	436	10	Q39073
43	215.5	7.3	419	5	Q77212
44	215	7.3	417	5	Q94740
45	215	7.3	443	10	Q40794

## ALIGNMENTS

RESULT	ID	Q9LQV6	PRELIMINARY:	PRT:	648 AA.
AC	Q9LQV6				
DT	01-OCT-2000	(Tremblrel. 15, Created)			
DT	01-OCT-2000	(Tremblrel. 15, Last sequence update)			
DT	01-DEC-2001	(Tremblrel. 19, Last annotation update)			
DE	F1086.15.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	Eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,				
RA	Williams S., Alcafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,				
RA	Hansen N.F., Huizar L., Kremetskaia I., Lenz C., Li J., Liu S.,				
RA	Lutero S., Rowley D., Schwartz J., Tortum M., Vysotskaia V., Yu G.,				
RA	Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;				
RT	*Genomic sequence for Arabidopsis thaliana BAC F1086 from chromosome				
RT	I.;				
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Ecker J.R.;				
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Ecker J.R.;				
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Chen R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,				
RA	Khan S., Kim C., Alcafi H., Bel B., Chin C., Chou J., Choi E.,				
RA	Lee J., Lenz C., Li J., Liu A., Liu S., Hansen N., Howing B., Koo T., Lam B.,				
RA	Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,				
RA	Thaveri A., Tortum M., Vaysberg M., Yu G., Davis R., Federspiel N.,				

RA Theologis A., Becker J.:  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC006917; AF79244.1; -  
 DR HSSP: P30274; IVIN.  
 DR InterPro: IPR004366; Cyclin.  
 DR SMART: SM00385; CYCLIN.2.  
 SO SEQUENCE 648 AA; 73432 MW; 3CB4AD8CA6B7EFE CRC64;

Query Match 96.8%; Score 2858; DB 10; Length 648;  
 Best Local Similarity 94.3%; Pred. No. 4.7e-182;  
 Matches 565; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

OY 6 MNSKRKPEPTPEFGKLRSLRKRRAQISPVLYOSPLMSKQIGVSAVSDCSDLAD 65  
 DB 1 MNSKRKPEPTPEFGKLRSLRKRRAQISPVLYOSPLMSKQIGVSAVSDCSDLAD 60  
 OY 66 DNVGCGSSRVKSSNPKKTLEVEVSKPGYNKFTIGSKRRTRRSKLRKKEGDE 125  
 DB 61 DNVGCGSSRVKSSNPKKTLEVEVSKPGYNKFTIGSKRRTRRSKLRKKEGDE 120  
 OY 126 IEVSESSCVDSNGAGLRRLNVKGNKINDDEISFSRDVTFAGHVSNSRLNFESENKE 185  
 DB 121 IEVSESSCVDSNGAGLRRLNVKGNKINDDEISFSRDVTFAGHVSNSRLNFESENKE 180  
 OY 186 SDVSVISGVGYCKFGSVTGADNDEIETSKPSSFEVADSSLGSAKELKPLEIVGCVS 245  
 DB 181 SDVSVISGVGYCKFGSVTGADNDEIETSKPSSFEVADSSLGSAKELKPLEIVGCVS 240  
 OY 246 DLASEKFESEVSLSLDESEDSORSELYSOYSDPDYSDYTPSIFPDGSEFSEKSSDSP 305  
 DB 241 DLASEKFESEVSLSLDESEDSORSELYSOYSDPDYSDYTPSIFPDGSEFSEKSSDSP 300  
 OY 306 ISHSRSLYLQFKFOCRSTIPNDFGSSCEEIEHSELRFPDDEVESESYRLERERSHAY 365  
 DB 301 ISHSRSLYLQFKFOCRSTIPNDFGSSCEEIEHSELRFPDDEVESESYRLERERSHAY 360  
 OY 366 MRDCAKAYCGRMDTGLIPRLRSIMOWIVK----- 396  
 DB 361 MRDCAKAYCGRMDTGLIPRLRSIMOWIVKPEEYLSLMLNLRMYOSAMIFVADCL 420  
 OY 397 -----QCSMDGLQDETFLGVGLDLRFLSKSFKSERLLILVGIASLTATRIEENOPYN 451  
 DB 421 PDYKQCSMDGLQDETFLGVGLDLRFLSKSFKSERLLILVGIASLTATRIEENOPYN 480  
 OY 452 SIKRRNTTNLRYSRREVYAMEMLYOEVLNFCETPTTFNLWLYTLAARANPEVERKA 511  
 DB 481 SIKRRNTTNLRYSRREVYAMEMLYOEVLNFCETPTTFNLWLYTLAARANPEVERKA 540  
 OY 512 KSLAVTSLSDOTOLCFMPSTVAALVLAACIEHNKISAYORVTKVHRTTNELPECVK 570  
 DB 541 KSLAVTSLSDOTOLCFMPSTVAALVLAACIEHNKISAYORVTKVHRTTNELPECVK 599

RESULT 2  
 ID 081794 PRELIMINARY; PRT: 429 AA.  
 AC 081794;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE CYCLIN 2B PROTEIN.  
 GN F8D20.130 OR AT4G35620.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Koetter P., Hempel S., Entlan K.-D., Hohnel J., Jesse T.,  
 RA Heljten L., Vos P., Mewes H.W., Mayer K.F.X., Scheller C., Beyer M.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rose M., Hempel S., Entlan K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.  
 DR EMBL: AL031135; CAZ20032.1; -  
 DR EMBL: AL161587; CAB80278.1; -  
 DR HSSP: P30274; IVIN.  
 DR InterPro: IPR004366; Cyclin.  
 DR InterPro: IPR004367; Cyclin\_C.  
 DR Pfam: PF00134; cyclin; 1.  
 DR Pfam: PF02984; cyclin; 1.  
 DR SMART: SM00385; CYCLIN.2.  
 DR PROSITE: PS00292; CYCLINS; 1.  
 KW Cell cycle; Cell division; Cyclin.  
 SO SEQUENCE 429 AA; 49786 MW; 5BDEBD7171A2FE09 CRC64;

Query Match 9.5%; Score 281.5; DB 10; Length 429;  
 Best Local Similarity 27.3%; Pred. No. 6.9e-11;  
 Matches 94; Conservative 69; Mismatches 134; Indels 47; Gaps 13;

OY 248 ACSEKSESEVSLSLDESEDSORSELYSOYSDPDYSDYTPSIFPDGSEFSEKSSDSPS 307  
 DB 72 SCQKKRLDSLNPST-SRQDEYTKLRKPSGNFEG-----DQIFDEEEKNEEYTLQPPMP 125  
 OY 308 HS-RSLYLQFKFOCRSTIPNDFGSSCEEIEHSELRFPDDEVESESYRLERERSHAY 364  
 DB 126 MSLEPYIEF-----DPMEEYEMDM---BEQDEPVLDDIYDANNISLA 168  
 OY 365 ---YMRDCAKAT-----CSRMD-----NGLPRLRSIMOWIVKQCSMDGLQDTFL 410  
 DB 169 AVEYVODLYDFYKTERFSCVPLDYMAQEDISCKMRAIIDLIEVHDKFELMNETFL 228  
 OY 411 GVGLDLRFLSKSFKSERLLILVGIASLTATRIE-NOPYNSIKRRNTTNLRYSRRE 469  
 DB 229 TVNLIDRFLSKQAV-ARKKLOVGLVALLACKYEVSVP---IVDLVVISDKATRTD 284  
 OY 470 VVAMEMLYOEVLNFCETPTTFNLWLYTLAARANPEVERKASLAVTSLSDOTOLCFMP 529  
 DB 285 VLEMEXIMSLTQFMNSLPDTPFLKRLKAQSDKRLTLASLTFLALVDYEMVRYP 344  
 OY 530 STVAALVLA-CIEHNKISAYORVTKVHRTTNELPECVKSL 572  
 DB 345 SLAAATVYTAQCTIHG-FSEMNSTCEFHCHYSENLLECCRRM 387

RESULT 3  
 ID 039070 PRELIMINARY; PRT: 429 AA.  
 AC 039070;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE CYCLIN 2B PROTEIN (FRAGMENT).  
 GN CYC2B.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-COLUMBIA; TISSUE=CELL SUSPENSIONS;  
 RX MEDLINE=95062258; PubMed=7972055;  
 RA Ferreira P.C.G., Hemery A.S., De Almeida Engler J., Bergounioux C.,  
 RA Bussens S., Van Montagu M., Engler G., Inze D.;  
 RT Three discrete classes of Arabidopsis cyclins are expressed during  
 RT different intervals of the cell cycle.\*;

[illegible]



```

Db 64 SPNIT-----VCNOKRAVLKDYNTNTLAESIITBEGNVACK-----ROGKETK 108
Oy 212 EIEISKPSSEYVADSSUGSAKELPELEIVGCVSLACSEKSESVSOLDESSEQRSE 271
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 109 QIE---EGLVDV---GEKSLAEDLSKIRW-----SLLASASKOLV 148
Oy 272 IYOSYSDYDYDPTSEFFSGSEKSSDSPISHSRSLYLQFQECRCSTIPNDGS 331
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 149 DCAEDRSDYDTCVOYIDISGV-----DPOFC-----SLYAA 182
Oy 332 SCEEFH-SELLRPDDEVEBSYLRLRERSHAY-----RQCAKAYSRMDNTGLPRL 386
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 183 STYDSINVAEL-----EORPSTSYMVQVRD-----IDFTM 213
Oy 387 RSIWQWLVKCCSDMGLOQETLFLVGLDLRPLSKGSEKSEKERTLLIVGLATRIEE 446
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 214 RCLLDMLVSESEKVLSDTLVTLVNLIDRPMHMYIEKQ-LQLLGTICLLASKEE 272
Oy 447 NOPYSIKRNF-10NLRISRHEVAMEVLVOELNFKCPTPTJPNELMFLYLAARANP 505
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 273 ---ISAPRIEEPCFTJDTMTYTRLEVLSEMLKVLNLSHFRLSVPTTKTFLRRIRAAQASD 329
Oy 506 -----EVERKAKSLAVTSLSDPOLCFMPTVAALVYA 540
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 330 KVLLEMELVANYRAELITPTTFLRLPSLIAASAVFLA 369

RESULT 8
Oy 015996 PRELIMINARY; PRT; 458 AA.
AC 015996;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CYCLIN A.
GN HECTA.
OS Hemictrotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidae; Euechinoidae; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemictrotus.
OX NCBI_TaxID=7650;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurokawa D., Akasaka K., Mitsunaga-Nakatsubo K., Shinada H.;
RT "Cloning of Cyclin A cDNA of sea urchin, Hemictrotus pulcherrimus.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AB008364; BAA22991.1; -.
DR HSSP: P30274; IYIN.
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR InterPro: IPR003013; HLM_Myc.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 2.
DR PROSITE: PS0038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 458 AA; 51308 MW; DFF9A14A2C68A63 CRC64;

Query Match 8.38; Score 246; DB 5; Length 458;
Best Local Similarity 27.79; Pred. No. 1.7e-08;
Matches 114; Conservative 61; Mismatches 156; Indels 80; Gaps 17;
Oy 179 FESKESDVAVISGVYCSKPSGVGADNE-EIEISKPSSEYVADSSUGSAKELPE 237
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 78 FQDENAH-----SRIGKGRFCILPSAGAAPAFSTHVDTTSSYVSSRS----- 120
Oy 238 LELVGVSDLACSEKSESVSDSLDDESS-----EORSEIYSQYDF-DYSPYTSIFPD 291
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 121 -----TSIKSTCKENHI--LLDNALSLPVPQORIPRLT---FPVEENNNVSL--- 164
Oy 292 SGSEFSEKSSDSPISHSRSLYLQFQECRCSTIPNDGSSCEEIHSLLRFDDEVEAE 351

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Db 165 --NEFSLTSSEFSPMLDLSL-----DAKCISPRVDT-----FDLSGEPTAAE 208
Oy 352 SYLRLRER----SHAYMRDCAKAYSRMDNTGLIPRLSIWQWLVKCCSDMGLOET 407
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 209 IYQYLKTAESKHKRKHGMYR-----KOPDITN--SMRCILVDMVSESEYRLNER 258
Oy 408 LELVGLDLRPLSKGSEKSEKERTLLIVGLATRIEENOPYSIKRNFNTIONLYSR 467
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 259 LYLAAPLIDRFLSMQSYLRAK-LQLVGTASMTVASKYEELTPPV--KEFYITDDYTSI 315
Oy 468 HEVAMEVLVOELNFKCPTPTJPNELMFLYLAARANPEVERKAKSLAVTSLSDPOLCF 527
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 316 KQVLRMEHLITKLVSEDLAPVINSFLPRFLAAQANSKTEHLIQYLAELTDEYDFIKY 375
Oy 528 WPTVAALVLAICTENHKISAVORYIKVHRTTNELPE--CYKSLDML 575
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 376 APSMTAASAVCLA-----NHTLNNEBMTPTMAHTTYQIGDIYPCVQDLHQL 422

RESULT 9
Oy 039068 PRELIMINARY; PRT; 429 AA.
AC 039068;
DT 01-NOV-1995 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CYCLIN 2A PROTEIN.
GN CYC2A.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA; TISSUE=CELL SUSPENSION;
RX MEDLINE=95062258; PubMed=7972055;
RA Ferreira P.C.G., Hemeryly A.S., De Almeida Engler J., Bergonjoux C.,
RA Bursens S., Van Montagu M., Engler G., Inze D.;
RT "Three discrete classes of Arabidopsis cyclins are expressed during
RT different intervals of the cell cycle.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11313-11317 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA; TISSUE=CELL SUSPENSION;
RA Van Montagu M.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: Z31400; GA893275.1; -.
DR HSSP: P30274; IYIN.
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR InterPro: IPR003013; HLM_Myc.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 2.
DR PROSITE: PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 429 AA; 49232 MW; B88EB57E40ADBEC CRC64;

Query Match 8.28; Score 243.5; DB 10; Length 429;
Best Local Similarity 24.98; Pred. No. 2.3e-08;
Matches 91; Conservative 70; Mismatches 155; Indels 49; Gaps 9;
Oy 222 VVADSSUGSAKELPELEIVGCVSLACSEKSESVSDSLDDESSQORSIYSQYSPDY 281
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 57 VVKRKSLSKNOEEL-----GCQKKKRDLSRPVTSVSGVEETNKKKLKPSPSA 106
Oy 282 SDYPTSEFFSGSEKSSDSPISHS-RSLYLQFQECRCSTIPNDGSSCEEIHS 340
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 107 NDFGCIPTD-----EEBATLIDLPMPMSLEKPYTE-----ADPMEVEEME 146

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Db 216 QDTPSMALIVDMLVESECKYLOANTLSLYLLIDMLSKKICRER-LOLIGITCM. 274
OY 440 LATRIENOPYNISIRKBNFT-IONLARYSRHEVAMMVOEVLNFCPTPTTFNLFMYL 498
Db 275 IATRYEE---INADRIDKFCFIDONTYKEEVKLESIVLKSSSYOLFAPTRKTELRLRL 331
OY 499 KAARA-----NPEYERKAKSLAVTSLSDQOLCFMPSTAAALVYLA 540
Db 332 RAAQASIKRPSIELEYLANIYLAETLIMNGFLMFLPSMAASSVFLA 378

RESULT 12
O41731 PRELIMINARY; PRT: 424 AA.
ID 041731
AC 041731
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CYCLIN IIIZM.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Ponceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=873; TISSUE=EAR;
RX MEDLINE=9431698; PubMed=8041798;
RA Renaldi J., Colasanti J., Rime H., Yuan Z., Sundaresan V.;
RT "Cloning of four cyclins from maize indicates that higher plants have
RT three structurally distinct groups of mitotic cyclins.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7375-7379(1994).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL, U10076; AAA20236.1; -
DR HSSP, P30274; 1VIN.
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR Pfam: PF00134; cyclin_1.
DR SMART: SM00385; cyclin_C.1.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
KW SEQUENCE 424 AA; 47777 MW; C3AEFIDC53687F5 CRC64;
SQ

Query Match 8.2%; Score 241; DB 10; Length 424;
Best Local Similarity 21.9%; Pred. No. 3.3e-08;
Matches 94; Conservative 92; Mismatches 162; Indels 82; Gaps 15;
OY 178 NFESENKSDVAVSYISVEYC-----SKFSYVGADNEIETLSKSS-SFVEAD 225
Db 3 NLRSONCHOGG--AMBSGVKAPKANTNRRAUSDINKITIG--PHGLAVSKRLSEKPA 59
OY 226 SLSGARELKEPELIVGCVSDIACSEKFESEVSDS-----LDDESEKORSEIYSQSPD 280
Db 60 AAANARKDQ-----AGVGHPRVTRKFAATLATQTVALLDPISGRKR-----NAD 107
OY 281 VSDTPTSPFDSDSESEKSSSDPSHSRLYQKRFQCFGSTIPNDGSCCEETISE 340
Db 108 TAFHTPA-----DMESTKMTDPSL-----PVSSEMDMSPE 140
OY 341 LLRPDEVEESYLRLRERSHA-----YMRDCAKAYCSMDNTGLP----- 384
Db 141 LKEIEMEDIEEAPDIDSGAGNSIADVDEIYRFY-RKTEGASCYVTNYSQTDIN 199
OY 385 -RLRSINWOMIVKQCSMGIOQETFLVGGLDRFLSKSFSKSERILLIVGASITLATR 443
Db 200 EKMGILIDMLIEHYKLELLETLFLVNIIDRLFLARENVKRL-LOLAGVTALLACK 258
OY 444 IEE-NOPYNSIRKRNFTIONLARYSRHEVAMMVOEVLNFCPTPTTFNLFMYLKAAR 502
Db 259 YEEVSVP-----VEDLILCDRAYTRADILEMERHRIIVNTLFNMSVFPFCFMRRLKAAQ 315

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OY 503 ANVEYERKAKSLAVTSLSDQOLCFMPSTAAALVYLAIEHNRISAVORYKIVHRTD 562
Db 316 SEKKLELSEFMEIETLSVEYEMLOFCPSMLAAALYTAQCTINERKSKNCKELHRTYSE 375
OY 563 NELPECVKSL 572
Db 376 EHLVCSRM 385

RESULT 13
O9SHPL PRELIMINARY; PRT: 429 AA.
ID O9SHPL
AC O9SHPL
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PUFATIVE CYCLIN 2.
DE AR2G17620.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Beall C.R., Ketchum K.A., Lee J.J., Rouning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umagay L., Tallon L.J., Gill J.E.,
RA Adams M.D., Cartea A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
RA Coppenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL, AC007509; AAD32949.1; -
DR HSSP, P30274; 1VIN.
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR Pfam: PF00134; cyclin_1.
DR SMART: SM00385; cyclin_C.1.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
KW SEQUENCE 429 AA; 49242 MW; B6E2DCFC4DE65770 CRC64;
SQ

Query Match 8.1%; Score 239.5; DB 10; Length 429;
Best Local Similarity 24.9%; Pred. No. 4.3e-08;
Matches 91; Conservative 70; Mismatches 155; Indels 49; Gaps 9;
OY 222 VPADSSLSGARELKEPELIVGCVSDIACSEKFESEVSDSLDDESEKORSEIYSQSPDY 281
Db 57 VNKRGSILSNKQFEER-----GCQKKKFLSLRPSVYRSGVEETRKKLKPSVSPA 106
OY 282 SDTPTSPFDSDSESEKSSSDPSHS-RLYIQKRFQCFGSTIPNDGSCCEETISE 340
Db 107 NDGDCIFTD-----EEETLIDLPMPMSLEKPYE-----ADPEEVEEM 146
OY 341 LRFDEVEESYLRLRERSHAYMRDCAKAYCSMDNTGLP-----RLRS 388
Db 147 DVTVEEPIVDIVLDSKNSIAAVEYVQD-LYAFRTMERFSCVVDVYMQQIDILNEKRA 205
OY 389 IMVQWIVKQCSMGIOQETFLVGGLDRFLSKSFSKSERILLIVGASITLATTRIEE-N 447

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2002, 14:22:26 : Search time 13.46 Seconds

(without alignments)  
1662.697 Million cell updates/sec

Title: US-09-821-839-2

Perfect score: 2952  
1 MKETAMRSKRKRPEPTFAAG.....RTDNLPECKVSLDLGLQ 578

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	262.5	8.9	434	1 CG2B_MEDVA	P46278 medicago va
2	253.5	8.6	328	1 CG2B_MEDSA	P46277 medicago sa
3	244	8.3	428	1 CG2B_MEDVA	P46277 medicago va
4	233.5	7.9	419	1 CG2B_ORISA	P40671 oryza sativ
5	227.5	7.7	341	1 CG2A_DAUCA	P25010 daucus caro
6	223.5	7.6	473	1 CG2A_ANTVA	P24800 antirrhinum
7	222.5	7.5	257	1 CG22_SOYBN	P25012 glycine max
8	220	7.5	426	1 CG2A_PATVU	P24861 patella vul
9	217.5	7.4	392	1 CG22_RANVA	P47827 rana japoni
10	217.5	7.4	415	1 CG2A_XENLA	P25028 xenopus lae
11	213	7.2	454	1 CG21_SOYBN	P25011 glycine max
12	212.5	7.2	421	1 CG21_MOUSE	P461426 mus musculu
13	212	7.2	422	1 CG2A_SPTSO	P41962 spissula sol
14	211	7.1	421	1 CG2A_MESAU	P37881 mesocricetu
15	210.5	7.1	406	1 CG2A_BOVIN	P30274 bos taurus
16	209	7.1	418	1 CG2A_XENLA	P18606 xenopus lae
17	207.5	7.0	432	1 CG2A_HUMAN	P20248 homo sapien
18	206	7.0	430	1 CG21_MOUSE	P24860 mus musculu
19	202	6.8	441	1 CG22_ANTVA	P34801 antirrhinum
20	201	6.8	420	1 CG2A_CHYRA	P31986 chlorofydra
21	201	6.8	465	1 CG21_HUMAN	P18396 homo sapien
22	200	6.8	395	1 CG2A_CHICK	P43449 gallus gall
23	199.5	6.8	409	1 CG2B_ARBPV	P37818 arabacia pun
24	199.5	6.8	399	1 CG2B_CHICK	P29332 gallus gall
25	199.5	6.8	422	1 CG2A_MOUSE	P18193 mus musculu
26	197	6.7	482	1 CG23_SCHPO	P10815 schizosacch
27	196	6.6	439	1 CG21_MESAU	P37882 mesocricetu
28	195	6.6	398	1 CG2A_HUMAN	P35067 homo sapien
29	194.5	6.6	423	1 CG21_RAT	P30277 rattus norv
30	194	6.6	398	1 CG22_MOUSE	P30126 mus musculu
31	193.5	6.6	428	1 CG2B_ARATH	P30183 arabidopsis
32	191.5	6.5	397	1 CG21_XENLA	P13350 xenopus lae
33	191.5	6.5	436	1 CG2B_DICDI	P42524 dictyostell

34	191	6.5	433	1 CG21_HUMAN	P14635 homo sapien
35	191	6.5	460	1 CG24_YEAST	P24871 saccharomyc
36	190	6.4	429	1 CG21_CRITLO	O08301 cricetus
37	189.5	6.4	428	1 CG2B_SPTSO	P13952 spissula sol
38	189	6.4	491	1 CG2A_DROME	P14785 drosophila
39	187.5	6.4	403	1 CG2B_CHICK	P39963 gallus gall
40	187	6.3	392	1 CG2B_XENLA	P13351 xenopus lae
41	187	6.3	478	1 CG21_EMENI	P30284 emericella
42	184.5	6.2	391	1 CG21_CARAU	Q92161 carassius a
43	184.5	6.2	404	1 CG22_HUMAN	O96020 homo sapien
44	183.5	6.2	388	1 CG2B_MARGL	P15206 marthasteri
45	179.5	6.1	404	1 CG22_MOUSE	Q92238 mus musculu

## ALIGNMENTS

RESULT 1  
CG2B\_MEDVA STANDARD: PRT: 434 AA.  
ID CG2B\_MEDVA  
AC P46278;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE G2/mitotic-specific cyclin 2 (B-like cyclin) (CYC2).  
OS Medicago varia.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.  
OX NCBI\_TaxID=36902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. A2;  
RA MEDLINE=95375541; PubMed=7647566;  
RA Meskiane I., Boegre L., Dahl M., Pirck M., Ha D.T.C., Swoboda I.,  
RA Heberle-Bors E., Ammerer G., Hirt H.;  
RT CYC2, a novel B-type alfalfa cyclin gene, is induced in the  
RT G0-to-G1 transition of the cell cycle.\*;  
RL Plant Cell 7:759-771(1995).  
CC -I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M  
CC (MITOSIS) TRANSITION.  
CC -I- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A  
CC SKRINE/THRONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS  
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS  
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.  
CC -I- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS  
CC ABRUPTLY DESTROYED AT MITOSIS.  
CC -I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.  
CC  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL: X82040: CAA57560.1: -  
CC HSPSP: P20248: 1FNI  
CC InterPro: IPR000553: Cyclin.  
CC Pfam: PF00134: cyclin\_1.  
CC Pfam: PF02984: cyclin\_C\_1.  
CC SMART: SM00385: CYCLIN\_2.  
CC PROSITE: PS00292: CYCLINS; 1.  
CC Cyclic: cell cycle; cell division; Mitosis.  
CC SEQUENCE 434 AA: 49367 MW: 6446FA2681A4C32 CRC64;  
SQ

Query Match 8.9%; Score 262.5; DB 1; Length 434;  
Best Local Similarity 27.0%; Pred. No. 6.9e-09;  
Matches 86; Conservative 57; Mismatches 112; Indels 63; Gaps 8;  
QY 292 SGSPFSEKSSSDSPISHSRSLYQFREQCRSTINPDGSSC----- 333

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DB 92 SQAATKRNKSNLN-----LMEFKNSTAIIDELKSPDEPEPMTL 133
OY 334 --EEHISELIRFDEEVEE-----SYLRLEERSHAYMDCAKAYC- 374
DB 134 EHTPEHMSDPLEMEVEEMEDIEGEMILDIDSCDANNSLAVVEYIEDLHAYRIKIELYCCV 193
OY 375 --SHMD-NTGILPLRLSINVMQIVKOCSDMGLQOETLFLGVGLDRFLSKGSKFSKSERPLI 431
DB 194 SPYMDQDGLDINEMRAILVDMLEIVHDKFDLMQETLFLTVNLIDRLAKONVVRK-LQ 252
OY 432 LVGLASLTATRIIE-NQPYNSIRKRNFTQNLRYSRHEVAVEMUVOEVLNFKCFTPTI 490
DB 253 LVGLVAMLLACKKEEVSVP---VSDLIHIDRAVYTRKDIEMERKMLNTLQYNSLPTA 309
OY 491 FNPLFLYKARANEVEERRAKSLAVTSLSDQTOLCFMPSTVAALVYLACIEHNKISAY 550
DB 310 YVFRRLFKAAQADKLELVAFLVLDLSEYEMLEKPPSLVAAAAYTAQCTVSGFKHM 369
OY 551 QVATKVHVRTDNEIPEC 568
DB 370 NKCEMHTNTSEDDLEEC 387

RESULT 2
CG2B_MEDSA STANDARD; PRT; 328 AA.
ID CG2B_MEDSA P30278:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DB G2/mitotic-specific cyclin 2 (B-like cyclin) (CYCNS2) (Fragment).
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93104677; PubMed=1307238;
RA Hirt H., Mink M., Pfosser M., Boegre L., Gyoergye J., Jonak C.,
RA Gaertner A., Dauts D., Heberle-Bors E.;
RT "Alfalfa cyclins: differential expression during the cell cycle and
RT in plant organs.";
RL Plant Cell 4:1531-1538(1992).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC -1- (MITOSIS) TRANSITION
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SKRINE/THERONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED IN ORGANS WITH DIVIDING CELLS.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X68741; CAA48675.1; -
CC PIR: S29925; S29925.
CC PIR: P00490; P00490.
CC HSSP: P20248; IJSD.
CC InterPro: IPR000553; Cyclin.
CC Pfam: PF00134; cyclin_1.
CC Pfam: PF02984; cyclin_2.
CC SMART: SM00385; CYCLIN; 2.
CC PROSITE: PS00292; CYCLINS; 1.

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KM Cyclin: Cell cycle; Cell division; Mitosis.
FT NON_TER 1
SQ SEQUENCE 328 AA; 37710 MW; 7E4CCB16B5D949E CRC64;

Query Match
Best local similarity 8.6%; Score 252.5; DB 1; Length 328;
Matches 78; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

OY 335 EEHISELIRFDEEVEE-----SYLRLEERSHAYMDCAKAYC---S 375
DB 31 EHTPEHMSDPLEMEVEEMEDIEGEMILDIDSCDANNSLAVVEYIEDLHAYRIKIELYCCV 90
OY 376 RMD-NTGILPLRLSINVMQIVKOCSDMGLQOETLFLGVGLDRFLSKGSKFSKSERPLI 434
DB 91 YDEQDLDERRAILVDMLEIVHDKFDLMQETLFLTVNLIDRLAKONVVRK-LQV 149
OY 435 IASLTATRIIE-NQPYNSIRKRNFTQNLRYSRHEVAVEMUVOEVLNFKCFTPTI 493
DB 150 LVAMLLACKKEEVSVP---VSDLIHIDRAVYTRKDIEMERKMLNTLQYNSLPTA 206
OY 494 LWFYKARANEVEERRAKSLAVTSLSDQTOLCFMPSTVAALVYLACIEHNKISAY 553
DB 207 MRFELKAAQADKLELVAFLVLDLSEYEMLEKPPSLVAAAAYTAQCTVSGFKHM 266
OY 554 IKVHVRTDNEIPEC 568
DB 267 CEWHRTVSEDDLEEC 281

RESULT 3
CG2B_MEDSA STANDARD; PRT; 428 AA.
ID CG2B_MEDSA P46277:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB G2/mitotic-specific cyclin 1 (B-like cyclin) (CYCNS1).
OS Medicago varia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=36902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV_A2; PubMed=7647566;
RX MEDLINE=9373541; PubMed=7647566;
RA Meskine I., Boegre L., Dahl M., Pirck M., Ha D.T.C., Swoboda I.,
RA Heberle-Bors E., Ammerer G., Hirt H.;
RT "CYCNS3, a novel B-type alfalfa cyclin gene, is induced in the
RT G0-to-G1 transition of the cell cycle.";
RL Plant Cell 7:759-771(1995).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC -1- (MITOSIS) TRANSITION
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SKRINE/THERONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X82039; CAA57559.1; -
CC HSSP: P20248; IJSD.
CC InterPro: IPR000553; Cyclin.

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DR EMBL: X62819; CAAA4631.1; -  
 DR PIR: S16521; S16521.  
 DR HSSP: P20248; 11SU.  
 DR InterPro: IPR000553; Cyclin.  
 DR Pfam: PF00134; cyclin\_C; 1.  
 DR SMART: SM00385; CYCLIN; 2.  
 DR PROSITE: PS00292; CYCLINS; 1.  
 DR Cyclin; cell cycle; cell division; Mitosis.  
 KW NON TER  
 SQ SEQUENCE 341 AA; 38724 MW; 5708DF4269C06F3F CRC64;

Query Match 7.7%; Score 227.5; DB 1; Length 341;  
 Best Local Similarity 27.7%; Pred. No. 6.3e-07;  
 Matches 89; Conservative 51; Mismatches 106; Indels 75; Gaps 14;

OY 298 EKSSSDSPISHRSRLYL-ORKEQFC-----RSTINDFGSSCEEHISELRFDD 346  
 DB 19 EISNNSSAVSNGEDLCREFEYKPCYAOKKRKGVEDYDVPGE-----KDD 67  
 OY 347 EEVEES-----YLRLREERSHA-----YMRDCAKAYCSRMNDNTGLIPRLSIWOMIV 395  
 DB 68 PQMSAAVSDVETELKQEMETKRRPMNNIDYQVDVTSNM-----RGVLDVWL 118  
 OY 396 KQCSDMGLQOETFLVGLDLRFLSKGSEKERTLLVGLSLATRIENOPNSTRK 455  
 DB 119 EVSLLEYLLEPTELTLAISYVDRLSYNVLNROK-LQLLGVSFLASKYEELKPKN--V 174  
 OY 456 RNFT-IONLKYSHREYVAMENLVQEVNLKRCFPTPLFNLMTYLAARANPEV-----ER 509  
 DB 175 ADEVDITDNTYSGQEVVEMADLTKLKEFGSPVKTGLG-IRAVENPDVPLKDEF 233  
 OY 510 KAKSLATVTSIDTQCLFNPSTVAALVLA-----CIEHNKISAQVRIKAVH 558  
 DB 234 LANYLAELSLDLGCLFVPSLIAAVTFLARTIRPNVNPWSIALQCSGK----- 286  
 OY 559 RTTNEPPECVKS-LDWLQ 578  
 DB 287 ---SKDLKECVLLHDLQMKR 304

RESULT 6  
 CG21\_ANTMA STANDARD; PRT: 473 AA.  
 ID CG21\_ANTMA  
 AC P34800;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE G2/mitotic-specific cyclin 1.  
 OS Antirrhinum majus (Garden snapdragon).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.  
 OC NCBI\_TaxID=4151;  
 RX MEDLINE=94148008; PubMed=8313906;  
 RA Fobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;  
 RT "Patterns of cell division revealed by transcriptional regulation of  
 RT genes during the cell cycle in plants."  
 RL EMBL J. 13:616-624(1994).  
 CC FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M  
 CC (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2  
 CC AND ARE ABRUPTLY DESTROYED AT MITOSIS.

CC -1- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM  
 CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT  
 CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.  
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS  
 CC ABRUPTLY DESTROYED AT MITOSIS.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.  
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DR EMBL: X76122; CAA53728.1; -  
 DR PIR: S41709; S41709.  
 DR HSSP: P30274; 1YIN.  
 DR InterPro: IPR000553; Cyclin.  
 DR Pfam: PF00134; cyclin\_C; 1.  
 DR SMART: SM00385; CYCLIN; 2.  
 DR PROSITE: PS00292; CYCLINS; 1.  
 DR Cyclin; cell cycle; cell division; Mitosis.  
 KW CYCLIN  
 SQ SEQUENCE 473 AA; 52704 MW; 502CF1735587638A CRC64;

Query Match 7.6%; Score 223.5; DB 1; Length 473;  
 Best Local Similarity 20.9%; Pred. No. 1.7e-06;  
 Matches 98; Conservative 99; Mismatches 182; Indels 89; Gaps 18;

OY 128 VBSGCVDSNSAGLRRLNVGNKINDDELISFRSVPVTFAGVNSNRSINFESEKESD 187  
 DB 7 VQOQNAEFAAVGAKKKNINAGEKN-----RRLGLDIGNLVYRGV---DQKAA 54  
 OY 188 VYSYISGV--EYCSNF--GSVYGGADNEETISKPSFYEA--DSLSGSAK----- 232  
 DB 55 IPQVSRPVTRSFCAQULANAOYAAADNNKIN-AGALVYDVGVLPRDVAARAPPAQKAA 113  
 OY 233 ELKPELEIGCVSDLCSEKSESEYSOSLDDESEQSEISQSYDPEYSDYPSIFPDS 292  
 DB 114 VVKPREELIVISPSVAEKKKEPIEKKAEKAKK-----APTL----- 155  
 OY 293 GSEPSKSSSDSPISHRSRLYLQREOPCRSTINDGSCSEEHISELRFDD-DEVE 351  
 DB 156 TSTLTARSKAASGVK-----TKKEQTV-----DIDAA--DVNNDLAUVLEVDMYK 200  
 OY 352 SYLRLREERSHAYMRDCAKAYCSRMNDNTGLIP-----RLRSIMVOMIVKQCSDMGLQOET 407  
 DB 201 FYKSVENESRPHDY-----GQPEINEMKRALIDWLQVNHKFEISPE 246  
 OY 408 LFLVGLDLRFLSKGSEKERTLLVGLSLATRIENOPNSTRKRTTQINR 464  
 DB 247 LYLITNIDRYLASET-TIRELDLVGIGAMLISKYEELWAVEVHELV-----CISDT 300  
 OY 465 YSRHEVAMENLVQEVNLKRCFPTPLFNLMTYLAARANPEVERAKSLAVTSIDQ 524  
 DB 301 YSDKOILVWEKKTLGALBMYLTVLPYFLVRFKASMTDSVENNYFLAELGMMNYAT 360  
 OY 525 LCFWSTVAALVLAACENHNKISAYQRIKAVHRTDNLDPCCVSL 572  
 DB 361 LLYCSMTAAASVYARCTLNKAPFMETLQHLTGSESPQLMDCAKLL 408

RESULT 7  
 CG22\_SOYBN STANDARD; PRT: 257 AA.  
 ID CG22\_SOYBN  
 AC P25012;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE G2/mitotic-specific cyclin s13-7 (B-like cyclin) (Fragment).  
 OS Glycine max (Soybean).



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CG2_RANJA
ID CG2_RANJA STANDARD: PRT: 392 AA.
AC 093229;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G2/mitotic-specific cyclin B2.
DS CCNB2.
SN Rana japonica (Japanese redbellied frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=98332197; PubMed=9669534;
RA Ihara J., Yoshida N., Tanaka T., Mita K., Yamashita M.;
RT "Either cyclin B1 or B2 is necessary and sufficient for inducing
RT germinal vesicle breakdown during frog (Rana japonica) oocyte
RT maturation."
RL Mol. Reprod. Dev. 50:499-509(1998).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC or send an email to license@isb-sdb.ch).
CC
CC EMBL: AB005253; BAA32563.1; -.
CC HSSP: P20248; IJ50.
CC InterPro: IPR000553; Cyclin.
CC Pfam: PF00134; cyclin.1.
CC SMART: SM00385; CYCLIN.C.1.
CC PROSITE: PS00292; CYCLINS; 1.
CC Cyclin; Cell cycle; Cell division; Mitosis.
CC SEQUENCE 392 AA; 43960 MW; 5058C4F8351CC9C8 CRC64;
SQ
Query Match 7.4%; Score 217.5; DB 1; Length 392;
Best Local Similarity 28.6%; Pred. No. 3e-06;
Matches 83; Conservative 44; Mismatches 102; Indels 61; Gaps 11;
QY 315 QFQKPCRTGIPNDPSSCEDEE---HSELL-----RPFDEEVESYRLR 357
DB 82 QVEE---ASVPVMDVSMKEEELCOAFSEVSLNHVVDIDAEDGDNOLCSFVVVDIYVLR 138
QY 358 ERESNNAVMDCKAYCSMDNTGLIRLSIMVQIVKQCSMDLQOETFLVGGLDR 417
DB 139 ERE---VOOSIKORY---LDGMEINERBALIVDMILQVNSRFQFLEETLVMGLAMDR 191
QY 418 FL-----SKSFSERTLLNGASITLARTIEENOPNSIRKRF--IQNLKRSHEVY 471
DB 192 FLOVQPISTRK---LDLVGTSLLASKYEE---MYSPEVDAFAYITDNATTSQIR 242
QY 472 AMEVLVOEVLNFKCPTPTLNFELMFLKAAANPEVERKASLAVTSISDQTOLCFWSPT 531
DB 243 EMEETILRELKFDLGRPLDLHLFRASKACADAOHTLAKYLMETLVDEYEVHPRSE 302
QY 532 VAAALVAVLACIEHNKISAVORYIKV-----HVKTNDMELEPCVSL 572
DB 303 IAAALALCLA-----QKVLGVGSMGSIQHNHTGYTEEDLPITIKHI 342

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RESULT 10
ID CGA2_XENLA STANDARD: PRT: 415 AA.
AC P47827;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin A2.
DS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95278730; PubMed=7758942;
RA Howe J., Howell M., Hunt T., Newport J.;
RT "Identification of a developmental timer regulating the stability of
RT embryonic cyclin A and a new somatic A-type cyclin at gastrulation."
RL Genes Dev. 9:1164-1176(1995).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) AND THE G2/M (MITOSIS) TRANSITIONS.
CC -1- SUBUNIT: INTERACTS WITH THE CDK2 AND CDC2 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATE STEADILY DURING G2 AND IS ABRUPTLY
CC DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC
CC EMBL: X85746; CAA59748.1; -.
CC HSSP: P30274; IVIN.
CC InterPro: IPR000553; Cyclin.
CC Pfam: PF00134; cyclin.1.
CC SMART: SM00385; CYCLIN.C.1.
CC PROSITE: PS00292; CYCLINS; 1.
CC Cyclin; Cell cycle; Cell division; Mitosis.
CC SEQUENCE 415 AA; 46670 MW; B0D5300093A1764D CRC64;
SQ
Query Match 7.4%; Score 217.5; DB 1; Length 415;
Best Local Similarity 32.3%; Pred. No. 3.2e-06;
Matches 76; Conservative 34; Mismatches 76; Indels 49; Gaps 9;
QY 329 FGSSCEEIHEHSELRFDDEE-----VESYLRLRERE---RSHAYMRDCAKAY 373
DB 136 FGSPMDVSI-----VDEQKGVGCNNVADYAKEIHGYLRMEVCKKPRAGVMO----- 183
QY 374 CSRMONTGLIRLSIMVQIVKQCSMDLQOETFLVGGLDRPLSKSFSERTLLVY 433
DB 184 KQPIITG---MKRALIVDMVLVEGEYKRLQNETLVLANVYIDRFLSSSVLRG-LDLY 238
QY 434 GIASLTARTIEENOP-----YNSIRKRNFTIOMLRSHREVAMEMVLVOEVLNFKCF 486
DB 239 GTANALLASKRFEETIPPEVAEFVY-----ITDDYTKKQVLMKHELVLVKLVSPDLA 289
QY 487 TPTTFNFMFLKAAANPEVERKASLAVTSISDQTO-LCFWSPVAAALVYLA 540
DB 290 APTILQYINQTFQIHVYSPKVESLSMFLGELSLVDADPPLRLYIPVAAARVIA 344

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RESULT 11
CG21_SOYBN STANDARD; PRT: 454 AA.
ID CG21_SOYBN
AC P25011;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G2/mitotic-specific cyclin 513-6 (B-like cyclin).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxId=3847;
[1]
SEQUENCE FROM N.A.
RA STRAIN-CY, AKISENGOKU; TISSUE=ROOT;
RA MEDLINE=9130894; PubMed=1851125;
RA Hata S., Kouchi H., Suzuki T., Ishii T.;
RA "Isolation and characterization of cDNA clones for plant cyclins.";
RA EMO J. 10:2681-2688(1991).
RL -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X62820; CAA44632.1;
CC PIR: S16522; S16522.
CC DR HSSP: P30274; IYIN.
CC DR InterPro: IPR000553; Cyclin.
CC DR Pfam: PF00134; cyclin_1.
CC DR Pfam: PF02984; cyclin_C_1.
CC DR SMART: SM00385; CYCLIN_2.
CC DR PROSITE: PS00292; CYCLINS; 1.
CC CYCLIN: Cell cycle; cell division; Mitosis.
CC KW SEQUENCE 454 AA; 50094 MW; 54EB459656A7C10 CRC64;
SQ

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Query Match 7.28; Score 213; DB 1; Length 454;
Best Local Similarity 21.58; Pred. No. 6, 8e-06;
Matches 95; Conservative 91; Mismatches 190; Indels 66; Gaps 17;

147 VGNFRINNDISFSDVTFAGVNSRSINFESENKESDVAVSYISGEVCKFGSVTG 206
17 VGGGQOQKKNVAGNRKAL-GDIGLAVRGVAVKAPRITTSFGOLLAN-AQAA 74
207 GADNE---IEIKPSFVEADSSIGSAELKPELEIVGCVSDLACSKRSEVSDSLD 262
75 AADNKRKQACANVAGPAPV-ANGAVAAAPR-PSVKAYIVPKPEKXTDT-- 126
263 DESSORSEIISQYSDFD---YSDTPSIFPDSCSEFSEKSSSDPSISHSRLYLQFK 317
127 DASPKKEVLKDKRKGDNPKKSKHTLF-----SVLTARSKACGTTNKP-----K 174
318 EOPGCSITPNRFGSCSEFHSLLRPD-DEVEESYILRREHSHAMRCACAKYCSR 376
175 EGIIT-----DIDS---DVNLEAAVEYIDDIKYKTKLVENESRPHDYI----- 215
377 MONTGLIP-----RLNSINWQIVKQCSMDGLQOETFLGCVGLDRFLSKGFSKSRLLIL 432
216 ---GSGEINERMAIIVDWLIDVHTKFEISETIYLTINILDRPLAVKTV-PRREQL 270

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RESULT 12
CGAL_MOUSE STANDARD; PRT: 421 AA.
ID CGAL_MOUSE
AC Q61456;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin A1.
DE CCNA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
SEQUENCE FROM N.A.
RA STRAIN-BALB/C; TISSUE=Testis;
RA MEDLINE=96152200; PubMed=8565853;
RA Sweeney C., Murphy M., Kubelka M., Ravnik S.E., Hawkins C.F.,
RA Wolgemuth D.J., Garrington M.;
RA "A distinct cyclin A is expressed in germ cells in the mouse.";
RA Development 122:53-64(1996).
[2]
FUNCTION.
RA MEDLINE=99057346; PubMed=9843212;
RA Liu D., Matzuk M.M., Sung W.K., Guo Q., Wang P., Wolgemuth D.J.;
RA "Cyclin A1 is required for meiosis in the male mouse.";
RA Nat. Genet. 20:377-380(1998).
[3]
FUNCTION.
RA STRAIN=SWISS WEBSTER;
RA MEDLINE=99169070; PubMed=10068472;
RA Ravnik S.E., Wolgemuth D.J.;
RA "Regulation of meiosis during mammalian spermatogenesis: the A-type
RA cyclins and their associated cyclin-dependent kinases are
RA differentially expressed in the germ-cell lineage.";
RA Dev. Biol. 207:408-418(1999).
RL -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF THE CELL CYCLE AT THE
CC G1/S (START) AND G2/M (MITOSIS) TRANSITIONS. MAY PRIMARILY
CC FUNCTION IN THE CONTROL OF THE GERMLINE MITOTIC CELL CYCLE AND
CC ADDITIONALLY IN THE CONTROL OF MITOTIC CELL CYCLE IN SOME SOMATIC
CC CELLS.
CC -1- SUBUNIT: INTERACTS WITH THE CDK2 AND CDC2 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- SUBCELLULAR LOCATION: IN OOCYTES AT LEAST, IT ASSOCIATES WITH THE
CC SPINDLE DURING METAPHASE.
CC -1- TISSUE SPECIFICITY: TESTIS AND OVARIES.
CC -1- DEVELOPMENTAL STAGE: IN MALE GERM CELLS JUST PRIOR TO OR DURING
CC THE FIRST, BUT NOT THE SECOND MEIOTIC DIVISION.
CC -1- MISCELLANEOUS: CCNA1 -/MALES ARE STERILE DUE TO A BLOCK OF
CC SPERMATOGENESIS BEFORE THE FIRST MEIOTIC DIVISION, WHEREAS FEMALES
CC ARE NORMAL.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC
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Db	215	REFSSMSVLRGK-LQVGTAAAMLASKEEITPPEVAEEFY-----ITDDPYTRKQ	264
Qy	470	VVAMEMLVQEVLENKCEPTPTIENFL-WFYKAAARANPEVERKAKSLAVTSLSD-OTOLCF	527
Db	265	VLRMEHLVKVLAFLDAAPTINOFITQYFLHQPANCKVESLAMEFLGELSLIDADPYLKY	324
Qy	528	WPSYVAALVVLA	540
Db	325	LPSYIAAAAFHIA	337

Search completed: July 23, 2002, 14:26:22  
Job time: 236 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2002, 14:18:56 ; Search time 20.95 Seconds  
(without alignments)  
2651.057 Million cell updates/sec

Title: US-09-821-839-2

Perfect score: 2952

Sequence: 1 MKELAMRNKRKRPEPTPFAG.....RTDNELEPCVKSIDWLGQ 578

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	281.5	9.5	204667	cyclin 2b - Arabid
2	262.5	8.9	209706	cyclin cycM2, B-t
3	252.5	8.6	S29925	cyclin 2 - alfalfa
4	250	8.5	S56679	mitosis-specific c
5	242.5	8.2	209596	cyclin cyc3 - maize
6	241	8.2	D57742	cyclin III - maize
7	239.5	8.1	429	probable cyclin 2
8	236.5	8.0	210525	cyclin B1b-11 - ye
9	234.5	7.9	S65734	mitosis-specific c
10	233.5	7.9	203639	cyclin 2 - rice
11	233	7.9	B86339	protein F2D10.10 l
12	232.5	7.9	446	mitosis-specific c
13	229	7.8	210527	cyclin Bld-11 - ye
14	227.5	7.7	341	mitosis-specific c
15	227.5	7.7	454	mitosis-specific c
16	227	7.7	A96803	probable mitotic c
17	225	7.6	C57742	cyclin II - maize
18	223.5	7.6	459	cyclin B1c-11 - ye
19	223	7.6	S41709	mitosis-specific c
20	222.5	7.5	202746	cyclin A-like prot
21	222.5	7.5	S74672	mitosis-specific c
22	222	7.5	F96790	hypothetical prote
23	220	7.5	210361	cyclin, B-type - c
24	219.5	7.4	426	cyclin A - common
25	218.5	7.4	483	cyclin A-type (clo
26	217.5	7.4	215637	cyclin A2 - Africa
27	215	7.3	443	mitosis-specific c
28	215	7.3	482	cyclin A-type (clo
29	214	7.2	493	cyclin, A-type - c

30	213.5	7.2	469	2	T07672	cyclin a2-type, m1
31	213	7.2	454	2	S16522	mitosis-specific c
32	212	7.2	422	2	A26328	cyclin A - Atlanti
33	210.5	7.1	406	2	S24788	cyclin A - bovine
34	209.5	7.1	440	2	T07676	cyclin b1-type, m1
35	209.5	7.1	484	2	T07675	cyclin a2-type, m1
36	209	7.1	418	2	S11678	cyclin A - African
37	207.5	7.0	432	2	S49462	cyclin A - rice
38	207.5	7.0	432	2	S08277	cyclin A - human
39	207.5	7.0	461	2	D96835	probable cyclin, 4
40	206	7.0	430	2	A43285	cyclin B1 - mouse
41	204.5	6.9	384	2	T02968	cyclin A-type (clo
42	204.5	6.9	460	2	D96505	probable mitotic c
43	204	6.9	430	2	I48316	cyclin B1 - mouse
44	202.5	6.9	348	2	T07669	cyclin a1-type, m1
45	202	6.8	441	2	S41710	mitosis-specific c

#### ALIGNMENTS

RESULT 1  
T04667  
cyclin 2b - Arabidopsis thaliana  
N:Alternate names: protein F8D20.130  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 23-Apr-1999 #sequence-revision 23-Apr-1999 #text-change 21-May-1999  
C:Accession: T04667  
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mew  
submitted to the Protein Sequence Database, July 1998  
A:Accession number: 215381  
A:Accession: T04667  
A:Molecule type: DNA  
A:Residues: 1-429 <BEV>  
A:Cross-references: EMBL:AL031335  
A:Experimental source: cultivar Columbia; BAC clone F8D20  
C:Genetics:  
A:Map position: 4  
A:Introns: 22/1; 67/2; 87/2; 138/3; 184/3; 214/3; 288/3; 321/3; 381/2  
A:Note: F8D20.130  
C:Superfamily: cyclin  
C:Keywords: cell cycle control; cell division control; mitosis

Query Match 9.5%; Score 281.5; DB 2; Length 429;  
Best Local Similarity 27.3%; Pred. No. 3.6e-10;  
Matches 94; Conservative 69; Mismatches 134; Indels 47; Gaps 13;

Qy	248	ACSRKFSFEVSDSLDDESSRSEIYSQYSDPDYSDYTPSTIFDSSGSEFSKSSDSPIS	307
Db	72	SCDKKKDLSLHPSI-SRSQETKRLKPSGNERG-----DCLTIDEERKNEEVTLDQHP	125
Qy	308	HS-RLYLQFKEDFCRSTIPNDFGSSCEEIHSSEILRFDEFEVESYLRRLRERSHA--	364
Db	126	MSLEPPIEF-----DMEEEVEEMED---EEQEPVVIDIDEVDANNSIA	168
Qy	365	---TMRCCAKAY-----CSRMD---NTGLPRRSIMQWIKQCSMDGLQETFL	410
Db	169	AVEVQDLIDYFKTEREFCVPLDYMAQOFDSDSKRALIIMLEIVNDKPELMMETFL	228
Qy	411	GVGLIDRFLSKGSFKSRTLLVGLASLTPLATRIEE-NQPVNSIKRNFYQNLKYSNHE	469
Db	229	TVINIDFLSKQAV-ARKKLQVLGVALLLACKYEEVSV--IVEDLVVISDKKYTRTD	284
Qy	470	VVAEMNIVQEVLANKECTPTIFNLFVYKAARANEVRRKASLAVTSIDPOTLCFMP	529
Db	285	VLEHKKIMLSLQFNMSLPFOYPLKRLFKAAOSDKKLEILASFLDELALVDYEVKRP	344
Qy	530	STVAALVLA-CIEHNKISAYQVRIKVVHFTTNDLEPCVKS	572
Db	345	SLAATAVYTAQCTIHG-FSEMNSTCEFHCHVSENLLECCRRM	387





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Db 206 ILIMLEIYHDKPILNETFLIVNLDRLKSNQNMRRK-LQVLGVALLLACKYEVS 264
Qy 448 QPNYSIKRNFETIONLRYSHREYVAMEWLVQEVNFKCTPTTFNFMFLYKAAARANDPV 507
Db 265 VP---VVEDVLVLISDKAYTFENDVLEMEKMTSLQFNISLPTQYFPLKFLKAAQADKRC 321
Qy 508 ERKAKSLAVTSLSDQTOLCFMPSTVAAALVVLACIEHNKISAYQVRIKVVHTVNTNEPE 567
Db 322 EVLASFLIELALVEYEMLRPPSLAATSYTAACCTLDOSRKMNSTCEHCHYSQDIME 381
Qy 568 CVKSL 572
Db 382 CSRKL 386

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# RESULT 8

T10525  
 cyclin B1b-11 - yellow lupine  
 C:Species: Lupinus luteus (yellow lupine)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: T10525  
 R:Decker, J.; Jelenka, J.; Zaborowska, Z.; Legocki, A.B.  
 A:Title: Isolation and classification of a family of cyclin gene homologues in Lupinus  
 A:Reference number: 217072; MUID:97385338  
 A:Accession: T10525  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <DBC>  
 A:Cross-references: EMBL:U24193; NID:g3253134; PIDN:AAC61888.1; PID:g3253135  
 A:Experimental source: clone CycB1b-11  
 C:Superfamily: cyclin  
 C:Keywords: cell cycle control; cell division control; mitosis

Query Match 8.0%; Score 236.5; DB 2; Length 454;  
 Best Local Similarity 22.7%; Pred. No. 2.5e-07;  
 Matches 97; Conservative 71; Mismatches 189; Indels 71; Gaps 11;

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Qy 147 VKGNKINDNDEISFSRDVTFAGHVSNSRSLNFESSEKSDVAVSYISGEVYKSGFSGVTG 206
Db 50 VKGNINILNPTIRSLCAQLAKAKAGENDKNLAIPTWTGPKPQVADGV--VAKRRVAPK 107
Qy 207 GADNEELIEIKSPSPVABSSLSAKELKPELEIVGCVSDLACSEKSEEVSDSIDDESS 266
Db 108 PAEKVTAKRPVEIVE---ISSGEVQDK-----SANKKKEGDALSKKKS 152
Qy 267 EORSEIYSQYSDYSDYTPIFPDGSEFSEKSSDSPISHSRSLYLQFKQFCRSTIP 326
Db 153 QTLTVLTANS-----KAAGLTETP-----KDOI-----ID 179
Qy 327 NDPSGSEEEIHSELLRPDEBEYESYLRLRERESHAYMRCAAYCRMDNGLIPRL 386
Db 180 IDAGDSNRELAAVEYI---EDMKFYKLAENENRPHQYD-----SOPENIERM 225
Qy 387 RSIWQWIVKQCSDMGLOETFLFGLDRFLSKGSFSEKSEFTLLVGLASLTATRIEE 446
Db 226 RALIVDLIDVQYKFDLSLETTLVLTINIVDRFLAVKTV-LRRELQVGVSMALMSKKEE 284
Qy 447 NOP--VYSIKRNFETIONLRYSHREYVAMEWLVQEVNFKCTPTTFNFMFLYKAAAR 504
Db 285 IMPEPVNDF---VCLDRAYTHQELVMEKTLIGLEWTLVPTTFEFLFRFIKASVPD 340
Qy 505 PEVERKAKSLAVTSLSDQTOLCFMPSTVAAALVVLACIEHNKISAYQVRIKVVHTVNTNE 564
Db 341 QELNMGHFLSELGMHMYATLVYCPSMVAASAVFAARCLTPIWNETLQLHNGYSEQ 400
Qy 565 LPECVKSL 572
Db 401 LMDCARLL 408

```

# RESULT 9

mitosis-specific cyclin 1b - Arabidopsis thaliana  
 N:Alternate names: B-type cyclin; group 1 cyclin  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 16-Jul-1999  
 C:Accession: S65734; S45293  
 R:Day, I.S.; Reddy, A.S.N.; Golovkin, M.  
 A:Title: Isolation of a new mitotic-like cyclin from Arabidopsis: complementation of  
 A:Reference number: S65734; MUID:96189269  
 A:Accession: S65734  
 A:Molecule type: mRNA  
 A:Residues: 1-445 <DAY>  
 A:Cross-references: EMBL:L27223; NID:g1360645; PIDN:AAB02028.1; PID:g1360646  
 R:Day, I.S.; Reddy, A.S.N.  
 A:Title: Cloning of a family of cyclins from Arabidopsis thaliana.  
 A:Reference number: S45293; MUID:94250688  
 A:Accession: S45293  
 A:Molecule type: mRNA  
 A:Residues: 213-276 <DAY>  
 A:Cross-references: EMBL:L27223  
 C:Genetics:  
 A:Gene: cyc1b  
 C:Superfamily: cyclin  
 C:Keywords: cell cycle control; cell division control; mitosis

Query Match 7.9%; Score 234.5; DB 2; Length 445;  
 Best Local Similarity 24.9%; Pred. No. 3.2e-07;  
 Matches 74; Conservative 67; Mismatches 133; Indels 23; Gaps 6;

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Qy 286 PSIFPDGSEFSEKSSSP-----ISHRSILYLQFKQFCRSTIPNDPSSCEEHSL 341
Db 119 PVEVETKKEVTKKEVAAVSPKKNKYTSVLSASK-----AACGVKPKPI 165
Qy 342 LRPDEVEEESTYLRLRERESHAYMRCAAYCSRMDNTGLIPRLSIWQWIVKQC 398
Db 166 IDIDSDCKNHLAAVEYDDMYSFYKEVEKSPRMVMIOTEMNKMRALLIDMLEVH 225
Qy 399 SDMGLOETFLFGLDRFLSKGSFSEKSEFTLLVGLASLTATRIEENQPNYSIKRNF 458
Db 226 IKFELMLETLVLTINIVDRFLSVKAV-PKRELQVGLISALLSKTEELNP-PQVNDLVY 283
Qy 459 TIONLRYSHREYVAMEWLVQEVNFKCTPTTFNFMFLYKAAARANDPEVERKAKSLAVTS 518
Db 284 VTDN-AYSRQILVMEKAILGNLEMYLTVPTQYVFLVRFIKASMSDPEENMHVFLAELG 342
Qy 519 LSDQTOLCFMPSTVAAALVVLACIEHNKISAYQVRIKVVHTDNDLPECVSLDL 575
Db 343 MNHYDTLTFPCSMQAAAVYTAARCLNKLSPAWDTLQPHGTETSEIMDSKLAPL 399

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# RESULT 10

cyclin 2 - rice  
 C:Species: Oryza sativa (rice)  
 C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 21-Jul-2000  
 C:Accession: T03675  
 R:Sauter, M.; Mehmedov, S.L.; Kende, H.  
 A:Title: Gibberellin promotes histone H1 kinase activity and the expression of cdc2 a  
 A:Reference number: 214999; MUID:95261415  
 A:Accession: T03675  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-419 <SAU>  
 A:Cross-references: EMBL:X82036; NID:g1694891; PIDN:CAA57556.1; PID:g1694892  
 A:Experimental source: cv. Pindaew53  
 C:Genetics:  
 A:Gene: cyc2  
 C:Superfamily: cyclin





C:Species: Lupinus luteus (yellow lupine)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: T10527  
 R:Deckert, J.; Jelenka, J.; Zaborowska, Z.; Legocki, A.B.  
 A:Title: Isolation and classification of a family of cyclin gene homologues in Lupinus  
 A:Reference number: 217072; MUID:9738538  
 A:Accession: T10527  
 A>Status: translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-452 <DEC>  
 A:Cross-references: EMBL:U44857; NID:g3253102; PIDN:AGC2425.1; PID:g3253103  
 A:Experimental source: cultivar ventus; clone cycbId-11  
 A:Superfamily: cyclin  
 C:Keywords: cell cycle control; cell division control; mitosis

Query Match 7.8%; Score 229; DB 2; Length 452;  
 Best Local Similarity 26.9%; Pred. No. 7.3e-07;  
 Matches 78; Conservative 56; Mismatches 120; Indels 36; Gaps 8;

OY 293 GSESEKSSDSPISHRS-----LYQKEQFCRSTIPNDFGSSCEEIHSLLRPDDE 347  
 DB 137 GGEKKKSRFLVTLVTRSKAAGLTNRKREKIDIDAGDSGNETAAVEYI-----E 188  
 OY 348 EVERSRYLRERERESHAYMRDCAKAYSRMDNTGLIPRLRSIMVOMIYQCSMDGLQDET 407  
 DB 189 DIVEFYRLAEENRPHQYMD-----SQPD--INEKRRALVLMVLINVHTKFDLSLET 238  
 OY 408 LFLVGLDLRFLSKGFSKSRRTILVGLASLTATRIEENQ-----YNSIKRNETTON 462  
 DB 239 LYIINIDIRFLAKTV-PRKELQVIGISIMLMAKYEIEIWPVEDEFVCLSDRAFI--- 294  
 OY 463 LRYSRHEVAMEMLVQEVLFNFKCFTPIFNFLMFYLLAKARAPVEERAKSLAVTSLSDQ 522  
 DB 295 -----HEVFLAMEKILIGKLEMTLTVPTPYVFLVTRFKASVPPQELNNAHFLSELGMHY 350  
 OY 523 TQLCFNSTYAALVYLACLEHKIKIAQYRIKAVRTINDLPCVKS 572  
 DB 351 GTLMWCPSMIAASAVPARCTLTKTPIMNETLKLHGYSKEQIMDCARLL 400

RESULT 14  
 S16521  
 mitosis-specific cyclin C13-1 - carrot (fragment)  
 N:Alternate names: A-type cyclin  
 C:Species: Daucus carota (carrot)  
 C:Date: 21-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 16-Jul-1999  
 C:Accession: S16521  
 R:Hata, S.; Kouchi, H.; Suzuki, I.; Ishii, T.  
 EMBL J. 10, 2681-2688, 1991  
 A:Title: Isolation and characterization of cDNA clones for plant cyclins.  
 A:Reference number: S16521; MUID:91330894  
 A:Accession: S16521  
 A:Molecule type: mRNA  
 A:Residues: 1-341 <HAT>  
 A:Cross-references: EMBL:X62819; NID:g18339; PIDN:CAA44631.1; PID:g829260  
 A:Superfamily: cyclin  
 C:Keywords: cell cycle control; cell division control; mitosis

Query Match 7.7%; Score 227.5; DB 2; Length 341;  
 Best Local Similarity 27.7%; Pred. No. 6.2e-07;  
 Matches 89; Conservative 51; Mismatches 106; Indels 75; Gaps 14;  
 OY 298 EKSSSDPSISHRSYL-OFKQFC-----RSTIPNDFGSSCEEIHSLLRPD 346  
 DB 19 EISNNSSAVSGNEDLLCRFEFVPCVAOKRRGKEDVGDEG-----KFDD 67  
 OY 347 EEVEES-----YLRLEERSHA-----YMRDCAKAYCSMDNTGLIPRLRSIMVOMIY 395  
 DB 68 PCMCASAVSVYETLQKQMEETKRRPMNYIQYQKDVTSNN-----KGYLVDMVLV 118

OY 396 KQSDMGLOEFLFLVGLDLRFLSKGFSKSRRTILVGLASLTATRIEENQPNYSIRK 455  
 DB 119 EVSEKLLPELTYLAISVDRYLSVNLNRK-LQLLGVSSFLIASKAEIRPKN---V 174  
 OY 456 RNFT-IQNLRYSRHEVAMEMLVQEVLFNFKCFTPIFNFLMFYLLAKARAPVE-----ER 509  
 DB 175 ADFVDTDMTVSQQEVKMEADLKLTFEKGSPVTVTFLOF-IRAOENPDVPRKLKFER 233  
 OY 510 KAKSLAVTSLSQGTQLCWPSVVAALVYLA-----CIENKISAYQRTIKVHV 558  
 DB 234 LANYLAELSLDYGLEVPVSLIASVTLARFTIRPNVPMWSIALQKCGYR----- 286  
 OY 559 RTVDNELPCCVKS-LDWLLQ 578  
 DB 287 ---SKDLKCVLLHLDLQGR 304

RESULT 15  
 A96803  
 probable mitotic cyclin a2-type [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
 C:Accession: A96803  
 R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Walzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: A96803  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-454 <STO>  
 A:Cross-references: GB:A8005173; NID:g11079479; PIDN:AGC29191.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F2P24.10  
 A:Map position: 1  
 A:Superfamily: cyclin

Query Match 7.7%; Score 227.5; DB 2; Length 454;  
 Best Local Similarity 24.8%; Pred. No. 9.1e-07;  
 Matches 105; Conservative 76; Mismatches 195; Indels 47; Gaps 14;

OY 172 SNRSRLNESEKESKEDVSVISGYEYCSKGSYTGADNEIETSRP---SSPVEADSL 228  
 DB 3 SSSRNLSQENPIPRNLAKTRTSLRDVGNRAPLGDITNKNRSPSSSTIVYNSMTI 62  
 OY 229 GSAKEL-KPELETGCVSDLACSKFSEEVSDSLDDESSQKSEIYSQISDFYSDYTPS 287  
 DB 63 GOSKRAPR-----ALSRNMVLGILDSGLPRPKPAKNITVPPEDLLOSDPS 111  
 OY 288 IFPDG---SESEKSSDSPISHRSYLQFKEQFCRSTIPNDFGSSCEEIHSLLRPD 345  
 DB 112 LICSPPALSLDASPTQOSPSTHDSLTNHYVYWEST--DDGDDDD--EYVND 166  
 OY 346 DEEVE-----ESTRLERERSHAHYMRDCAKAYCSMDNTGLIPRLRSIMVOMIY 396  
 DB 167 SLDMPOLCASFADYIEHLKVSVRNRPALD---YMETQSS-INASMRSLIDWIVE 221  
 OY 397 QCSDMGLOEFLFLVGLDLRFLSKGFSKSRRTILVGLASLTATRIEENQPNYSIRK 456  
 DB 222 VAEERYLSPELTYLAIVNVDRYL-GNAINKNOLLGTYCMIAAKYEE---VCYPOVE 277  
 OY 457 NRT-IQNLRYSRHEVAMEMLVQEVLFNFKCFTPIFNFLMFYLLAKARAPVE-----ERK 510  
 DB 278 DCYITDNTVYLRNELLEKESSVLYNLYLKFELTTPACFLRRFLRAAGRKEVPSLSRCL 337

Thu Aug 1 16:41:57 2002

us-09-821-839-2.rpr

Page 7

Oy	511	AKSLAATYSIDPTOLCFEWSRYAAALVVLCTE-HNKISAYORVKIVHRTTDDNEPCV	569
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Db	338	ACUTETSELSDYAMLRAPSLVAASAVFLAQYLTHFSRKRPWNALETHTSYRAHHMACV	397
		:	
Oy	570	KSL 572	
Db	398	KNL 400	

Search completed: July 23, 2002, 14:22:49  
Job time: 233 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2002, 14:18:35 ; Search time 14.67 Seconds

(without alignments)  
962.372 Million cell updates/sec

Title: US-09-821-839-2

Perfect score: 2952

Sequence: 1 MKEIMRNSKRKPEPEFAG.....RTTDNELPECVKSLDLGLQ 578

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201.5	6.8	432	1	US-08-522-166-8
2	201.5	6.8	432	1	US-08-488-382A-8
3	201.5	6.8	432	2	US-08-480-912-8
4	194	6.6	433	1	US-08-522-166-7
5	194	6.6	433	1	US-08-488-382A-7
6	194	6.6	433	2	US-08-480-912-7
7	188.5	6.4	430	2	US-08-460-694-3
8	188.5	6.4	430	3	US-08-460-744-3
9	188.5	6.4	430	3	US-07-667-711B-3
10	184.5	6.2	404	2	US-09-092-770-3
11	184.5	6.2	404	2	US-09-222-851-3
12	184	6.2	149	2	US-08-460-694-5
13	184	6.2	149	2	US-08-460-744-5
14	184	6.2	149	3	US-07-667-711B-5
15	183	6.2	173	1	US-08-193-977-4
16	179.5	6.1	403	2	US-09-092-770-4
17	179.5	6.1	403	4	US-09-222-851-4
18	168	5.7	492	1	US-08-463-090B-10
19	163.5	5.5	148	2	US-08-460-694-6
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21	163.5	5.5	148	3	US-07-667-711B-6
22	160	5.4	171	1	US-08-193-977-5
23	156.5	5.3	106	2	US-08-464-517-25
24	156.5	5.3	106	2	US-08-246-361A-25
25	156.5	5.3	106	3	US-08-463-772-25
26	156.5	5.3	106	5	PCT-US93-05000-25
27	156.5	5.3	295	2	US-08-464-517-20

28	156.5	5.3	295	2	US-08-246-361A-20	Sequence 20, Appl
29	156.5	5.3	295	5	US-08-463-772-20	Sequence 20, Appl
30	156.5	5.3	295	5	PCT-US93-05000-20	Sequence 20, Appl
31	155.5	5.3	295	1	US-07-947-120-8	Sequence 8, Appl
32	155.5	5.3	295	1	US-08-472-893A-8	Sequence 8, Appl
33	155.5	5.3	295	2	US-08-460-694-2	Sequence 2, Appl
34	155.5	5.3	295	3	US-08-460-744-2	Sequence 2, Appl
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36	155.5	5.3	295	3	US-08-947-492-8	Sequence 8, Appl
37	155.5	5.3	618	2	US-08-770-761A-3	Sequence 3, Appl
38	155.5	5.3	647	2	US-08-770-761A-8	Sequence 8, Appl
39	155.5	5.3	660	2	US-08-770-761A-2	Sequence 2, Appl
40	155.5	5.3	662	2	US-08-770-761A-5	Sequence 5, Appl
41	155.5	5.3	705	2	US-08-770-761A-7	Sequence 7, Appl
42	153.5	5.2	295	2	US-08-464-517-19	Sequence 19, Appl
43	153.5	5.2	295	2	US-08-246-361A-19	Sequence 19, Appl
44	153.5	5.2	295	3	US-08-463-772-19	Sequence 19, Appl
45	153.5	5.2	295	5	PCT-US93-05000-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-522-166-8  
Sequence 8, Application US/08522166  
Patent No. 5783661  
GENERAL INFORMATION:  
APPLICANT: Robert, J.M.; Ohtsuda, M.; Koff, A.C.; Cross, F.  
TITLE OF INVENTION: Human Cyclin E  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: Christensen, O'Connor, Johnson and Kindness  
STREET: 2800 Pacific First Center, 1420 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101-2347  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette-3.5 inch, 1.44MB storage  
COMPUTER: IBM PC Compatible/Pentium  
OPERATING SYSTEM: MS-Windows 3.1  
SOFTWARE: Word for Windows-6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/522,166  
FILING DATE: June 7, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,309  
FILING DATE: September 20, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Sheiness, Diana K.  
REGISTRATION NUMBER: 35,356  
REFERENCE/DOCKET NUMBER: FHR0-1-8597  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)  
TELEFAX: 1-206-224-0779  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: Cyclin B polypeptide sequence; Figure 3  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
US-08-522-166-8

Query Match 6.88; Score 201.5; DB 1; Length 432;  
Best Local Similarity 24.14; Pred. No. 7.8e-10;  
Matches 90; Conservative 67; Mismatches 136; Indels 81; Gaps 13;

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OY 209 DNEFIETSKPS-----SVEADSLGSAKELPELEIVGCVSLDACEKF----- 253
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Db 29 DQENINPEKAAVPOOPTRAALAVLAKSGNPRGLAQOORPRTIRAPLADLPVNDHVTVP 88
OY 254 -----SEEVSDSLD-DESSQRESEIYSQSDPYSDPTSFEDSG-----SE 295
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Db 89 PMKANSKOPAFIIVHDEAKEOKKPAESOKIERED---ALAFNSAISLPGRKFLVPLD 145
OY 296 FSEKSSSDPSHISRLYLQKQPCFRCSTTPNDGSSCEPHISELIRFDDDEVEESTLR 355
| : : : : | : : : : | : : : : | : : : : |
Db 146 YPMDSGSEPHIMDSIVLEDEKPVSVNEND-----YHBDIH-----TYLR 187
OY 356 LRERERSHAYMRDCAKAYCSRMNTGLIPRLRSIMVOIWKQSDMGLQOETFLGVL 415
| : : : : | : : : : | : : : : | : : : : |
Db 188 EMEVK-----CKPKVGYMKKOPDITNSMRALIVDMIVGEVEYKIQNETLHLAVNYI 239
OY 416 DRPLSGSEKSERLILVGIASLTLATRIEENP-----YNSIKRNFOTONLRYSRH 468
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Db 240 DRFLSSMSVLRGK-LQLVGTAAMLASKEFEIYPPVAAEFVY-----ITDDTYTKK 289
OY 469 EVVAMEMVLVOEVLNFKCFTPTIFNPL-WFYLKAARANPEVERAKSLAVTSLSD-QTOLC 526
| : : : : | : : : : | : : : : | : : : : |
Db 290 QVLIRHEHLIVLKVLPDIAAPVNOFLQYFLHOOPANCKVESIAMFLGELSLIDADPYLK 349
OY 527 FWPSTVAALVULA 540
| : : : : | : : : : | : : : : | : : : : |
Db 350 YLPSTVIAAGAAFLHA 363

RESULT 2
US-08-488-382A-8
; Sequence 8, Application US/08488382A
; Patent No. 5807698
; GENERAL INFORMATION:
; APPLICANT: Roberts, J.M.; Ohtsubo, M.; Koff, A.C.; Cross, F.
; TITLE OF INVENTION: Human Cyclin E
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.5 inch, 1.44mb storage
; OPERATING SYSTEM: MS-Windows 3.1
; SOFTWARE: Word for Windows-6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.382A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,309
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHRO-1-8600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
; TELEFAX: 1-206-224-0779
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
; ORIGINAL SOURCE:

```

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; ORGANISM: Homo Sapiens
; US-08-488-382A-8

Query Match
Best local similarity 24.1%, Score 201.5; DB 1; Length 432;
Matches 90; Conservative 67; Mismatches 136; Indels 81; Gaps 13;

OY 209 DNEFIETSKPS-----SVEADSLGSAKELPELEIVGCVSLDACEKF----- 253
| | | | | : : : : : | : : : : | : : : : | : : : : |
Db 29 DQENINPEKAAVPOOPTRAALAVLAKSGNPRGLAQOORPRTIRAPLADLPVNDHVTVP 88
OY 254 -----SEEVSDSLD-DESSQRESEIYSQSDPYSDPTSFEDSG-----SE 295
| : : : : | : : : : | : : : : | : : : : |
Db 89 PMKANSKOPAFIIVHDEAKEOKKPAESOKIERED---ALAFNSAISLPGRKFLVPLD 145
OY 296 FSEKSSSDPSHISRLYLQKQPCFRCSTTPNDGSSCEPHISELIRFDDDEVEESTLR 355
| : : : : | : : : : | : : : : | : : : : |
Db 146 YPMDSGSEPHIMDSIVLEDEKPVSVNEND-----YHBDIH-----TYLR 187
OY 356 LRERERSHAYMRDCAKAYCSRMNTGLIPRLRSIMVOIWKQSDMGLQOETFLGVL 415
| : : : : | : : : : | : : : : | : : : : |
Db 188 EMEVK-----CKPKVGYMKKOPDITNSMRALIVDMIVGEVEYKIQNETLHLAVNYI 239
OY 416 DRPLSGSEKSERLILVGIASLTLATRIEENP-----YNSIKRNFOTONLRYSRH 468
| | | | | : | | | : | | | : | | | : |
Db 240 DRFLSSMSVLRGK-LQLVGTAAMLASKEFEIYPPVAAEFVY-----ITDDTYTKK 289
OY 469 EVVAMEMVLVOEVLNFKCFTPTIFNPL-WFYLKAARANPEVERAKSLAVTSLSD-QTOLC 526
| : : : : | : : : : | : : : : | : : : : |
Db 290 QVLIRHEHLIVLKVLPDIAAPVNOFLQYFLHOOPANCKVESIAMFLGELSLIDADPYLK 349
OY 527 FWPSTVAALVULA 540
| : : : : | : : : : | : : : : | : : : : |
Db 350 YLPSTVIAAGAAFLHA 363

RESULT 3
US-08-480-912-8
; Sequence 8, Application US/08480912
; Patent No. 5861259
; GENERAL INFORMATION:
; APPLICANT: Roberts, J.M.; Ohtsubo, M.; Koff, A.C.; Cross, F.
; TITLE OF INVENTION: Immunassays for Detection of Human Cyclin E
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.5 inch, 1.44mb storage
; OPERATING SYSTEM: MS-Windows 3.1
; SOFTWARE: Word for Windows-6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.912
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,309
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHRO-1-8599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
; TELEFAX: 1-206-224-0779
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

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1  LENGTH: 432 amino acids
2  type: amino acid
3  STRANDEDNESS: single
4  TOPOLOGY: linear
5  MOLECULE TYPE: protein
6  DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
7  ORIGINAL SOURCE:
8  ORGANISM: Homo Sapiens
9  OS-08-480-912-8

```

Query Match	6.8%;	Score 201.5;	DB 2;	Length 432;
Best Local Similarity	24.1%;	Pred. No. 7.8e-10;		
Matches 90;	Conservative 67;	Mismatches 136;	Indels 81;	Gaps 13

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QY 209 DNEIELSPRS-----SPVEDSSLSGAKELPTELEJGVCSDLACSEKF----- 255
Db 29 DQENTPEKAAAPVQOPRTIRALAIYAKSGNPRGLAQQORPKTRRVAIPLDLPYNDEHYTP 88
QY 254 -----SEEVSDLSU--DESSQORSEIYSQSDPFDYSPTESIFPDS-----SE 295
Db 89 PMKANSGQAFITIHVDEAKEQKKPAESQKIEBD---ALNFMSALSLPGRRPIVPLD 145
QY 296 FSEKSSSDPISHSKSLYLQREOPCSTIPNDFGSCBEERHSELRLRDEVEEYSLR 355
Db 146 YPMDGFESEPHMDMSIYLEDKRPVSNNPD-----YHEDIH-----TYLR 187
QY 356 LRERESHAYMDDCAKACASNDMTUGLIRLRSTIMQYVKKCSDMKQGOETLPLGGL 415
Db 188 EMVK-----CKPKVGYMKKOPDITNSMRALIVDMVLVEGEEKKLONETLHLAVYI 239
QY 416 DRLSLGSEKSEKERTILVIGIALSLTLATRIEENP-----YNSIRKKNFTJONLRSH 468
Db 240 DRLSLGSEKSEKERTILVIGIALSLTLATRIEENP-----YNSIRKKNFTJONLRSH 468
QY 469 EVVAMENLVOEVLNFKCETPIIENFL-WFYLIKARANPEYERKANSLAVTSLSD-QFOLC 526
Db 290 QVTRMEHLYIKVLTIEDLAIPVNOFLQYFHOOAPNCKVESLAMELGETSLIDADPYLK 349
QY 527 FWPSTYAAALVVLVA 540
Db 350 YLPSVINGAAPHLA 363

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REGISTRATION NUMBER: 35,356  
REFERENCE/DOCKET NUMBER: PHRO-1-8597  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)  
TELEFAX: 1-206-224-0779  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 433 amino acids  
type: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: Cyclin A polypeptide sequence; Figure 1  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
US-08-522-166-7

Query Match	5.6%;	Score 194;	DB 1;	Length 433;
Best Local Similarity	22.2%;	Pred. No. 3.7e-09;		
Matches	87;	Conservative	64;	Mismatches 169; Indels 72; Gaps 14;

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QY 170 HVENSMULFESEKNEDSVAVIS--GEVECSNFGSVTGGANNEIELISKSSSVLEADS 2277
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 NAENKARIMAGAKRYPPAPAAATSKPGIRPRTALIGDI--SNKVSFQIQAEMPKKAPSA 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 LGSAA--KELKPELEIVGCVSLACSEKFSFEVSDISLDDSSSQRSEIYSQXSDFDYSDYT 285
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 TGVAYIDKKLPKLEKVPYMLVAVPVYSEVYPPPEPEPEPEPEYKKEK-----LS 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 286 PS--TFPDGSEFSEKSSSSDSPISHSRSYLAQFKQFCRSTIPNDFGSCCEEIHSELLRF 3444
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 PEPILVDTFASPMETSGCACA-----EEOQLQA-----FSDVILAV 153
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 DDEVEE-----SYLRLRERERBSHAIIMRCAKAYCSRMNDTGLIPRLRSI 389
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 154 NDDVADIEDGADPNLCSEYBKDIYALYLRQLEEEQA-----VRKRYLLBREVV---NNRAI 204
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 MVOMIYKQCSDMGILQOETPLFLGVLIDRFSLSKGS--FKSRPTLLVIGIASILATRIENQ 448
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 LIDMLVQVQMKRLLQOETRMVTVSILIDRFQNNCKYK--KMQLQVGVIAAMKIASKEEYF 262
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 PYNISIKRNFETJONLRYSRHFEVAMEMVLQOEVLFNFCFTPTIFNFLMYLKAARANPEVE 508
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 263 P-PEIGDFAFVTDN--TYRKHQIRQMEKKILRLAINFGIGRPLHFLRLASKIGEVKEQH 320
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 RKAASIAVTSISDQTOQLCFWSTVYAAALVILA 540
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 321 TLAKYLMELITMLDYDMVHFPPSOILAAGAFCLA 352
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: FILING DATE: June 7, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/764,309
: FILING DATE: September 20, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Shelness, Diana K.
: REGISTRATION NUMBER: 35,356
: REFERENCE/DOCKET NUMBER: FHO-1-8600
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
: TELEFAX: 1-206-224-0779
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 433 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: DESCRIPTION: Cyclin A polypeptide sequence; Figure 3
: ORIGINAL SOURCE:
: ORGANISM: Homo Sapiens
: US-08-488-382A-7

```

```

Query Match          6.6%; Score 194; DB 1; Length 433;
Best Local Similarity 22.2%; Pred. No. 3.7e-09;
Matches 87; Conservative 64; Mismatches 169; Indels 72; Gaps 14;

```

```

QY 170 HVSNSRLNFESEKESDVSVIS--GVYCSKFGSVTGADNEIEISKPSFVEADSS 227
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 NAEKKAKINMAGAKRVPAPATSKPGLRPRALGDI--GNKVSQLOAKPMKKEAKPSA 70
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 LGSA--KELPELEIVGCVSDLACSEKSEFEVSDSLDDESSQORSEIYSQYSDFDYDT 285
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 71 TGVKIDKRLKPLEKVPMLVPVSEVPPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE 116
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 286 PS-IFPDSGSESEKSSSDSPISHSRLYLQFKQFCRSTIPNDGSSCEEIHSLLRF 344
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117 PEPTLVDTASPSPMETSGCAPA-----EQLCOA-----FSDVILAV 153
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 DDEVEE-----SYLRLEKERSHAYMRDCAKAYCSRMNTGLIPRLSI 389
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 154 NDVADGADPNLCSEYBKDIYAYLRQLEEQA-----VRPKYLLBREVTG---NMRAI 204
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 MWQIVVQCSMDGLOQELFLGVGLDRLSKGS--FKSERILLINGIASITLARIENQ 448
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 205 LIDMLVQVMKFRLLQETMTVSTIDRFQNNCVFK--KMLQLVGVTAMFTASKEEY 262
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 PYSIRKRNFTIQLRYSRHEVYVAMEMLVQELNFKCFTPTIFNLFMYLKAARANEVE 508
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 263 P-PEIDGFAYVDN--TYTKHQIRQMEKILRALNFGIGRPLPLHFRASKIGEYKVEQH 320
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 RKAKSLAVTSLSQDTQCFMPSTVAALVYLA 540
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 321 TLAKYLMELTMDYDMVHPPSQIAAGAFCLA 352
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 6
US-08-480-912-7
: Sequence 7, Application US/08480912
: Patent No. 5851259
: GENERAL INFORMATION:
: APPLICANT: Roberts, J.M.; Ohtsubo, M.; Koff, A.C.; Cross, F.
: TITLE OF INVENTION: Immunoassays for Detection of Human Cyclin E
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
: STREET: 2800 Pacific First Center, 1420 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98101-2347

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette-3.5 inch, 1.44mb storage
: COMPUTER: IBM PC Compatible/Pentium
: OPERATING SYSTEM: MS-Windows 3.1
: SOFTWARE: Word for Windows-6.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/480,912
: FILING DATE: June 7, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/764,309
: FILING DATE: September 20, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Shelness, Diana K.
: REGISTRATION NUMBER: 35,356
: REFERENCE/DOCKET NUMBER: FHO-1-8599
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
: TELEFAX: 1-206-224-0779
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 433 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: DESCRIPTION: Cyclin A polypeptide sequence; Figure 3
: ORIGINAL SOURCE:
: ORGANISM: Homo Sapiens
: US-08-480-912-7

```

```

Query Match          6.6%; Score 194; DB 2; Length 433;
Best Local Similarity 22.2%; Pred. No. 3.7e-09;
Matches 87; Conservative 64; Mismatches 169; Indels 72; Gaps 14;

```

```

QY 170 HVSNSRLNFESEKESDVSVIS--GVYCSKFGSVTGADNEIEISKPSFVEADSS 227
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 NAEKKAKINMAGAKRVPAPATSKPGLRPRALGDI--GNKVSQLOAKPMKKEAKPSA 70
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 LGSA--KELPELEIVGCVSDLACSEKSEFEVSDSLDDESSQORSEIYSQYSDFDYDT 285
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 71 TGVKIDKRLKPLEKVPMLVPVSEVPPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE 116
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 286 PS-IFPDSGSESEKSSSDSPISHSRLYLQFKQFCRSTIPNDGSSCEEIHSLLRF 344
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117 PEPTLVDTASPSPMETSGCAPA-----EQLCOA-----FSDVILAV 153
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 DDEVEE-----SYLRLEKERSHAYMRDCAKAYCSRMNTGLIPRLSI 389
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 154 NDVADGADPNLCSEYBKDIYAYLRQLEEQA-----VRPKYLLBREVTG---NMRAI 204
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 MWQIVVQCSMDGLOQELFLGVGLDRLSKGS--FKSERILLINGIASITLARIENQ 448
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 205 LIDMLVQVMKFRLLQETMTVSTIDRFQNNCVFK--KMLQLVGVTAMFTASKEEY 262
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 PYSIRKRNFTIQLRYSRHEVYVAMEMLVQELNFKCFTPTIFNLFMYLKAARANEVE 508
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 263 P-PEIDGFAYVDN--TYTKHQIRQMEKILRALNFGIGRPLPLHFRASKIGEYKVEQH 320
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 RKAKSLAVTSLSQDTQCFMPSTVAALVYLA 540
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 321 TLAKYLMELTMDYDMVHPPSQIAAGAFCLA 352
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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```

RESULT 7
US-08-460-694-3
: Sequence 3, Application US/08460694
: Patent No. 5858655
: GENERAL INFORMATION:
: APPLICANT: Arnold, Andrew
: TITLE OF INVENTION: PRADI Cyclin and its cDNA
: NUMBER OF SEQUENCES: 8

```



```

1 CLASSIFICATION: 435
2 ATTORNEY/AGENT INFORMATION:
3 NAME: McConathy, Evelyn H.
4 REGISTRATION NUMBER: 35,279
5 REFERENCE/DOCKET NUMBER: 0609,4070005
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 202-371-2500
8 TELEFAX: 202-371-2540
9 INFORMATION FOR SEQ ID NO: 3:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 150 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: not relevant
14 TOPOLOGY: linear
15 MOLECULE TYPE: peptide
16 US-08-460-744-3
17
18 Query Match 6.4%; Score 188.5; DB 3; Length 150;
19 Best Local Similarity 36.5%; Pred.No. 2,2e-09;
20 Matches 58; Conservative 24; Mismatches 58; Indels 19; Gaps 5
21
22 QY 386 LRSIMVOMIRKQSDSGDLOEFTLEFGVGLIDRFLSKSGFSKSEKRLILVAGLSLTLATRIE 445
23 1 MRALIVMLIVEVEBEKRLQNEFLMLAVNTIDFLSSMSVLERK-LQLVGPAAMLAKKEE 59
24
25 QY 446 ENDP-----YNSIKRNFTTQNLKRYSHREYVAMWLVQELNFKCFPTIINFY-WFY 497
26 60 ELPPEVAEVEFY-----ITDDTYRKQVLRREHIVLKVLFEDLAPLVNQFLQYF 110
27
28 QY 498 LKARANPEVERKASLAVTSLS-D-OVOLCEPSTVAQA 535
29 111 LHQPANCKVESLAMPFLGELSLDADPLIKLIPSVINQA 149
30
31 RESULT 9
32 US-07-667-711B-3
33 Sequence 3, Application US/07667711B
34 Patent No. 6110700
35 GENERAL INFORMATION:
36 APPLICANT: ARNOLD, ANDREW
37 TITLE OF INVENTION: Prad1 cyclin and its cDNA
38 NUMBER OF SEQUENCES: 8
39 CORRESPONDENCE ADDRESS:
40 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
41 STREET: 1100 NEW YORK AVE., NW, SUITE 600
42 CITY: WASHINGTON
43 STATE: DC
44 COUNTRY: USA
45 ZIP: 20005
46 COMPUTER READABLE FORM:
47 MEDIUM TYPE: Floppy disk
48 COMPUTER: IBM PC compatible
49 OPERATING SYSTEM: PC-DOS/MS-DOS
50 SOFTWARE: PatentIn Release #1.0, Version #1.30
51 CURRENT APPLICATION DATA:
52 APPLICATION NUMBER: US/07/667,711B
53 FILING DATE: 11-MAR-1991
54 CLASSIFICATION: 435
55 ATTORNEY/AGENT INFORMATION:
56 NAME: MCPHAIL, DONALD R.
57 REGISTRATION NUMBER: 35,811
58 REFERENCE/DOCKET NUMBER: 0609,4070000
59 TELECOMMUNICATION INFORMATION:
60 TELEPHONE: (202) 371-2600
61 TELEFAX: (202) 371-2540
62 INFORMATION FOR SEQ ID NO: 3:
63 SEQUENCE CHARACTERISTICS:
64 LENGTH: 150 amino acids
65 TYPE: amino acid
66 STRANDEDNESS: single
67 TOPOLOGY: not relevant
68 MOLECULE TYPE: peptide

```

US-07-667-711B-3

Query Match 6.4%; Score 188.5; DB 3; Length 150;  
 Best Local Similarity 36.5%; Pred. No. 2.2e-09;  
 Matches 58; Conservative 24; Mismatches 58; Indels 19; Gaps 5;

QY 386 LRSIMQWIVYKQCSMDGLQOETFLFVGLDLRFLSKGSPKSEPTLLIVGLASLTARIE 445  
 DB 1 MRALVMDLVEGEVEEYKIQNETLHLAVNTIDRELSMSVLRKQ-LQVLTAALMLASKFE 59  
 QY 446 ENDP-----YNSIKRNFITQNLKYSRHEVYAMENVQEVLENKCEFTPIFNFL-WFY 497  
 DB 60 EIVPEVAERVY-----ITDDTYTKQVLRMEHLVVLKFTDLAAPTVOFLQYF 110  
 QY 498 LKAARANPEVERKAKSLATYSLD-QTOLCFEPPSTVAAA 535  
 DB 111 LH00PACVKESLAFMLGELSLDADPYLKLPSVYAGA 149

RESULT 10

US-09-092-770-3  
 ; Sequence 3, Application US/09092770  
 ; Patent No. 5973119  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Coats, Steven R.  
 ; APPLICANT: Bass, Michael B.  
 ; APPLICANT: Robinson, Murray O.  
 ; TITLE OF INVENTION: No. 5973119e1 Cyclin E Genes and Proteins  
 ; FILE REFERENCE: A-524  
 ; CURRENT APPLICATION NUMBER: US/09/092,770  
 ; CURRENT FILING DATE: 1997-06-05  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 404  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-092-770-3

Query Match 6.2%; Score 184.5; DB 2; Length 404;  
 Best Local Similarity 21.7%; Pred. No. 2.4e-08;  
 Matches 84; Conservative 72; Mismatches 148; Indels 83; Gaps 13;

QY 215 ISKPSFVEA-DSSLSAKELKPELEIVGCVSDLACSEKSESEVSLSLDESSDQRESEY 273  
 DB 1 MSRRSSRLQAKQOPQPSQTESPQEAQII-----QAKKRKTQVKKRREEVTKKHQYEIR 55  
 QY 274 SOYSDPFYSDYTSIFPDSGSESEKSSDSPISHRSLSLYLQFKDQPCFRTIPNDFGSSC 333  
 DB 56 NCMPVPLSGISPCITIE--TPHKEIGTSD-----FSRFTYRKFNLFNPSPLDLSMGC 109  
 QY 334 EEIHSLELRFDDDEVEBSYLRLREKRSNAYMDCKAKYCCRMNDTGLIRLSIMQW 393  
 DB 110 SKEVWLMNKKESRYVHDKHFEVL-----HSDLEPQMRSLIDW 148  
 QY 394 IVKCSMDGLQOETFLFVGLDLRFLSKGSPKSEPTLLIVGLASLTARIE-NQPYNS 452  
 DB 149 LLEVCVEYTLHREFTYLAODFDRFMFLQKIDINKNMLQIGISLFLASKLEIYAP--- 205  
 QY 453 IRRKNFTQNLRY-----SRHEVYAMENVQEVLENKCEFTPIFNFLFYK--AARAN 504  
 DB 206 -----KLOEFAVYTDGACSEEDILKRELITLAKLWELCPVTTISMLNLFQVNDALKA 259  
 QY 505 PEVERKAKS-----LAVTSLSDQTOLCFMPSTVAAALVVLACTIEHNKISA 549  
 DB 260 PKVLLPQYSQETFIQIAQLDLCLALDLSLEFYRI-----LTAALCHFTSIE----- 308  
 QY 550 YQRIKAVHVRTDNELPCEYKSLDWLL 576  
 DB 309 ---VVKRASGLEMDISSECV---DMNV 329

RESULT 11  
 US-09-222-851-3  
 ; Sequence 3, Application US/09222851  
 ; Patent No. 6165753  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Coats, Steven R.  
 ; APPLICANT: Bass, Michael B.  
 ; APPLICANT: Robinson, Murray O.  
 ; TITLE OF INVENTION: No. 6165753e1 Cyclin E Genes and Proteins  
 ; FILE REFERENCE: A-524  
 ; CURRENT APPLICATION NUMBER: US/09/222,851  
 ; CURRENT FILING DATE: 1998-12-30  
 ; EARLIER APPLICATION NUMBER: 09/092,770  
 ; EARLIER FILING DATE: 1998-06-05  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 404  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-222-851-3

Query Match 6.2%; Score 184.5; DB 4; Length 404;  
 Best Local Similarity 21.7%; Pred. No. 2.4e-08;  
 Matches 84; Conservative 72; Mismatches 148; Indels 83; Gaps 13;

QY 215 ISKPSFVEA-DSSLSAKELKPELEIVGCVSDLACSEKSESEVSLSLDESSDQRESEY 273  
 DB 1 MSRRSSRLQAKQOPQPSQTESPQEAQII-----QAKKRKTQVKKRREEVTKKHQYEIR 55  
 QY 274 SOYSDPFYSDYTSIFPDSGSESEKSSDSPISHRSLSLYLQFKDQPCFRTIPNDFGSSC 333  
 DB 56 NCMPVPLSGISPCITIE--TPHKEIGTSD-----FSRFTYRKFNLFNPSPLDLSMGC 109  
 QY 334 EEIHSLELRFDDDEVEBSYLRLREKRSNAYMDCKAKYCCRMNDTGLIRLSIMQW 393  
 DB 110 SKEVWLMNKKESRYVHDKHFEVL-----HSDLEPQMRSLIDW 148  
 QY 394 IVKCSMDGLQOETFLFVGLDLRFLSKGSPKSEPTLLIVGLASLTARIE-NQPYNS 452  
 DB 149 LLEVCVEYTLHREFTYLAODFDRFMFLQKIDINKNMLQIGISLFLASKLEIYAP--- 205  
 QY 453 IRRKNFTQNLRY-----SRHEVYAMENVQEVLENKCEFTPIFNFLFYK--AARAN 504  
 DB 206 -----KLOEFAVYTDGACSEEDILKRELITLAKLWELCPVTTISMLNLFQVNDALKA 259  
 QY 505 PEVERKAKS-----LAVTSLSDQTOLCFMPSTVAAALVVLACTIEHNKISA 549  
 DB 260 PKVLLPQYSQETFIQIAQLDLCLALDLSLEFYRI-----LTAALCHFTSIE----- 308  
 QY 550 YQRIKAVHVRTDNELPCEYKSLDWLL 576  
 DB 309 ---VVKRASGLEMDISSECV---DMNV 329

RESULT 12  
 US-08-460-694-5  
 ; Sequence 5, Application US/08460694  
 ; Patent No. 5858655  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arnold, Andrew  
 ; TITLE OF INVENTION: PRADI Cyclin and its cDNA  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P. L.L.C.  
 ; STREET: 1100 New York Avenue, N.W., Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,694  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McConathy, Evelyn H.  
REGISTRATION NUMBER: 35,279  
REFERENCE/DOCKET NUMBER: 0609.4070002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-694-5

Query Match 6.2% Score 184; DB 2; Length 149;  
Best Local Similarity 37.1%; Pred. No. 5,4e-09;  
Matches 56; Conservative 25; Mismatches 66; Indels 4; Gaps 3;

QY 386 LRSIMQWIVKQCSMDGLQETFLGVLDRFLSKSFKSERTLLIVGIASLTATRIE 445  
DB 1 MRCILVDMLEVESEEDKLRHETFLGCVNYIDRFISKISVLGRK-IQLVGAASMTLAKYE 59  
QY 446 ENQYNSIRKRNFTIONLRYSRHEVAMEMLVQEVINFCPTPTIFNFIPLFKARANP 505  
DB 60 EIVPPDV--KEFAYITDDTYTSQOVLRMHILIKVLPFDVAVPTTNMFCEDFLKSCDAD 117  
QY 506 EVERKAKSLAVTSLD-QTOLCFWPSYVAAA 535  
DB 118 KLSLTMFLTELIDMDAYLKPSTYAAA 148

RESULT 13  
US-08-460-744-5  
Sequence 5, Application US/08460744  
Patent No. 6107541  
GENERAL INFORMATION:  
APPLICANT: Arnold, Andrew  
TITLE OF INVENTION: PRADI Cyclin and its cDNA  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,744  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McConathy, Evelyn H.  
REGISTRATION NUMBER: 35,279  
REFERENCE/DOCKET NUMBER: 0609.4070005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-744-5

Query Match 6.2% Score 184; DB 3; Length 149;  
Best Local Similarity 37.1%; Pred. No. 5,4e-09;  
Matches 56; Conservative 25; Mismatches 66; Indels 4; Gaps 3;

QY 386 LRSIMQWIVKQCSMDGLQETFLGVLDRFLSKSFKSERTLLIVGIASLTATRIE 445  
DB 1 MRCILVDMLEVESEEDKLRHETFLGCVNYIDRFISKISVLGRK-IQLVGAASMTLAKYE 59  
QY 446 ENQYNSIRKRNFTIONLRYSRHEVAMEMLVQEVINFCPTPTIFNFIPLFKARANP 505  
DB 60 EIVPPDV--KEFAYITDDTYTSQOVLRMHILIKVLPFDVAVPTTNMFCEDFLKSCDAD 117  
QY 506 EVERKAKSLAVTSLD-QTOLCFWPSYVAAA 535  
DB 118 KLSLTMFLTELIDMDAYLKPSTYAAA 148

RESULT 14  
US-07-667-711B-5  
Sequence 5, Application US/07667711B  
Patent No. 6110700  
GENERAL INFORMATION:  
APPLICANT: ARNOLD, ANDREW  
TITLE OF INVENTION: Pradi Cyclin and its cDNA  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/667,711B  
FILING DATE: 11-MAR-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MCPHAIL, DONALD R.  
REGISTRATION NUMBER: 35,811  
REFERENCE/DOCKET NUMBER: 0609.4070000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2540  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 149 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-07-667-711B-5

Query Match 6.2% Score 184; DB 3; Length 149;  
Best Local Similarity 37.1%; Pred. No. 5,4e-09;  
Matches 56; Conservative 25; Mismatches 66; Indels 4; Gaps 3;  
QY 386 LRSIMQWIVKQCSMDGLQETFLGVLDRFLSKSFKSERTLLIVGIASLTATRIE 445

Search completed: July 23, 2002, 14:22:21  
Job time: 226 sec

DB 1 MRCILVDWLVVEEEDKLRERFLFGVNYIDRFPSKISVLRGK-LQLVGAASMLAKYE 59  
OY 446 ENQPVNSIKRNFNTIONLNSRHEVYAMWLVQEVNFKCPTPIFNFILFYTLKARANP 505  
DB 60 EIPRPV--KEFAYITDDYTSQVLRHEHLILKLVTFDVAVPTNMFCDEFLKSCDADD 117  
OY 506 EVERKAKSLAVTSLSLSD-OTQLCFWPSYVAAA 535  
DB 118 KIKSLTMFLTELIDMDAYLKLPSTTAAA 148

## RESULT 15

US-08-193-977-4  
; Sequence 4, Application US/08193977  
; Patent No. 5625031  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, KEVIN R.  
; APPLICANT: COLEMAN, KEVIN G.  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND  
; TITLE OF INVENTION: P34CDK2 CELL CYCLE REGULATORY KINASES AND HUMAN  
; TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: REED & ROBINS  
; STREET: 635 BRYANT STREET  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/193.977  
; FILING DATE: 08-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINS, ROBERTA L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5998-0016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 173 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-193-977-4

Query Match 6.2%; Score 183; DB 1; Length 173;

Best Local Similarity 33.3%; Pred. No. 8.4e-09; Matches 58; Conservative 25; Mismatches 69; Indels 22; Gaps 5;

OY 360 ERSNAYARD---CAKAYCSRMNDNTGLIPRLASIMYQWIVKOCSDMKLQOETLFLGVGLL 415  
DB 5 EDIHTYLRNEMEVCKRPVGYMKROPDITNSMRAILVDWLVEVGEYKLNQETLHLAVNYI 64  
OY 416 DRFLSKGSFSEKERTILLVGIASLTATRIENOP-----YNSIRKRNFTIQLNLYSRH 468  
DB 65 DRFLSSMSVLRGK-LQLVGTAAMVLASKEFEIYPRVAFVY-----ITDDTYTRK 114  
OY 469 EVVAMEMLVQEVNLFKCFPTPIENFL-WFLKAKARANPEVERKAKSLAVTSLSLSD 521  
DB 115 QVLRHEHLVLRKLVFLDLAAPTAVNOFLTQYFLHQPANCKVESLAWFLGELSLID 168.

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2002, 14:18:10 ; Search time 34.11 Seconds  
(without alignments)  
1882.165 Million cell updates/sec

Title: US-09-821-839-2  
Perfect score: 2952  
Sequence: 1 MKEIAMRNSKRKRPPTFAC.....RTYDNLPECVKSLDWILQ 578

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A: Geneseq\_032802: \*  
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT: \*  
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT: \*  
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT: \*  
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT: \*  
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT: \*  
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT: \*  
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT: \*  
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16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT: \*  
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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT: \*  
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT: \*  
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT: \*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2952	100.0	578	22	AAE12998
2	738	25.0	145	22	AAE12999
3	241.5	8.2	424	21	AAE12999
4	222	7.5	509	21	AAE12999
5	208.5	7.1	515	21	AAE12999
6	207	7.0	431	12	AAE12999
7	198.5	6.7	449	12	AAE12999
8	196	6.6	420	21	AAE12999
9	195	6.6	398	20	AAE12999
10	195	6.6	398	22	AAE12999
11	194	6.6	295	20	AAE12999

12	193	6.5	348	21	AAE12998
13	193	6.5	360	21	AAE12998
14	193	6.5	369	21	AAE12998
15	191	6.5	433	17	AAE12998
16	191	6.5	433	22	AAE12998
17	191	6.5	475	22	AAE12998
18	191	6.5	490	22	AAE12998
19	188.5	6.4	421	22	AAE12998
20	184.5	6.2	404	20	AAE12998
21	184.5	6.2	404	21	AAE12998
22	184.5	6.2	404	22	AAE12998
23	182	6.2	335	22	AAE12998
24	179.5	6.1	403	20	AAE12998
25	179.5	6.1	403	22	AAE12998
26	175	5.9	350	21	AAE12998
27	175	5.9	372	21	AAE12998
28	175	5.9	399	21	AAE12998
29	173.5	5.9	709	22	AAE12998
30	173.5	5.9	709	22	AAE12998
31	168.5	5.7	339	20	AAE12998
32	168.5	5.7	411	16	AAE12998
33	168	5.7	492	18	AAE12998
34	168	5.7	492	18	AAE12998
35	166.5	5.6	387	21	AAE12998
36	161.5	5.5	227	21	AAE12998
37	161.5	5.5	339	21	AAE12998
38	160.5	5.4	602	22	AAE12998
39	159	5.4	575	22	AAE12998
40	158	5.4	323	21	AAE12998
41	155.5	5.3	295	13	AAE12998
42	155.5	5.3	295	15	AAE12998
43	155.5	5.3	295	22	AAE12998
44	155.5	5.3	618	18	AAE12998
45	155.5	5.3	618	19	AAE12998

#### ALIGNMENTS

RESULT	ID	AAE12998	standard: Protein: 578 AA.
AC	AAE12998		
DT	28-JAN-2002	(first entry)	
DE	Arabidopsis thaliana	SDS protein.	
KW	Meiotic prophase I; chromosome 1; male sterile SDS mutant; apomixis;		
KW	Plant breeding; seed production; SDS protein.		
OS	Arabidopsis thaliana.		
FX	Key	Location/Qualifiers	
FT	Domain	361..521	
FT		/label= Cyclin_domain	
XX	WO200174144-A1.		
XX	11-OCT-2001.		
XX	29-MAR-2001; 2001WO-US09875.		
XX	31-MAR-2000; 2000US-193523P.		
XX	(UYPE-) UNIV PENNSYLVANIA STATE.		
XX	Ma H;		
XX	WPI: 2001-662939/76.		
XX	N-PDB: AAD21310.		

Arabidopsis thaliana  
Arabidopsis thaliana  
Arabidopsis thaliana  
Arabidopsis thaliana  
Human cyclin B1.  
Human polypeptide  
Human polypeptide  
Drosophila melanog  
Novel human diago  
Human cyclin E2 pr  
Human cyclin E2 pr  
Human cyclin E2 fu  
Drosophila melanog  
Mouse cyclin E2 pr  
Mouse cyclin E2 fu  
Arabidopsis thaliana  
Arabidopsis thaliana  
Arabidopsis thaliana  
Drosophila melanog  
Drosophila melanog  
Soybean cyclin del  
Schizosaccharomyce  
Cyb1 protein. Can  
Candida cyclin, Cy  
Arabidopsis thaliana  
Arabidopsis thaliana  
Arabidopsis thaliana  
Drosophila melanog  
Drosophila melanog  
Arabidopsis thaliana  
pradi. Homo sapie  
bcl-1 protein. Ho  
Human shear stress  
Human cyclin D1-hu  
Human cyclin D1/cy

PT A new plant gene from Arabidopsis, designated SDS, mutations in which  
 PT are associated with inability to produce pollen, is useful for the  
 PT production of male sterile plants for plant breeding -  
 XX  
 XX  
 PS Claim 7; Fig 1; 47pp; English.

CC The patent discloses novel plant gene from Arabidopsis thaliana,  
 CC designated SDS, which is associated with a failure to maintain  
 CC homologue attachment during meiotic prophase I. The SDS gene is  
 CC located on chromosome 1 and is useful in plant breeding to produce  
 CC male sterile SDS mutants and cloned progeny by apomixis where  
 CC meiosis is bypassed in seed production. The gene may also be  
 CC used as a probe to identify related genes in other plant species,  
 CC and to identify and isolate other genes of the meiosis regulatory  
 CC pathway. The present sequence is SDS protein from Arabidopsis thaliana.  
 CC  
 XX  
 XX

Sequence 578 AA:

Query Match 100.0%; Score 2952; DB 22; Length 578;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-244;  
 Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKETAMNSRKKEPTPEFAGKRLRSTRLRRRAQISPVLVQSPLMVKIGVSAASVSDSCS 60  
 DB 1 mkeiamnsrktkeptpefagkrlrstlrkraqispylvqspmlskqlysaasvds 60  
 QY 61 DLADDVSCGSSRVEKSSNPKKTLLEEVYSGKPYNNKETTGDSEKFRTRRSKLHKE 120  
 DB 61 dladdvscgssrveksnppkllleevsgkpynnvetlgydskfrtrrsykhkc 120  
 QY 121 KEGDEIVSESSCVDSNSGAGRLRLNKGKINDNDEISFSRSDVTFAHVSNSKSLMFE 180  
 DB 121 kegdelvsesscvsdmsgagrlrlnvkgklnndelsfsrsdvtfaghvsnslmfe 180  
 QY 181 SENESQYVIVIGVEYCSKFGSVTGCADNEFIETSKPSPFEANSSIGSAKELKPELET 240  
 DB 181 senesqvivigveycskfgsvtgcadnefietskpspfearssigsaekelpel 240  
 QY 241 VGCYSDLACSEKFESEVSDSLDSESEORSEIYSQSDPEYSDYTPSIFPDGSEFESEKS 300  
 DB 241 vgcysdlacsekfeesvdslddesesorseiysqsdpeydytpsfifdgsefseks 300  
 QY 301 SSQSPGHSRSTVLOPFKPCRCSTIPNDFGSGCEEHSEILRFNDEVEVSYLRLRPRE 360  
 DB 301 ssdspghsrstvlpfrkpcrcstipndfgsgceehseilrfndeevesylrlpre 360  
 QY 361 RSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQOETFLFGVGLDRPLS 420  
 DB 361 rshaymrdcakaycsrmdntgliprlrsimvwivkqcsdmglqgetlflgvglldrpls 420  
 QY 421 KGSFKSERTLLIVGLASLTATRIENOPYNSIRKRNFTIONLARSRHEVVAEMVLVOEV 480  
 DB 421 kgfskserllivglasltatrienopynsirkrnftionlarsrhevvaemvlvgev 480  
 QY 481 LNEKCFPTTFNPLMFLYKAAKARNPEVERKAKSLAVTSLSDOQTQLCFMPSTVAALVYLA 540  
 DB 481 lnecfpttfnplmflylkaarnpeverkakslavtslsdqtlqcfmpstvaaalvyla 540  
 QY 541 CIEHNKISAYORVIAKIVRTTONELPEGVKSLDMLLGO 578  
 DB 541 ciehnkisaygvrikvrttonelpegvksldwllgq 578

RESULT 2

AAE12999 ID AAE12999 standard; Protein; 145 AA.

XX AC AAE12999;

XX DT 28-JAN-2002 (first entry)

XX XX Arabidopsis thaliana SDS protein cyclin box.

XX XX Meiotic prophase I; chromosome 1; male sterile SDS mutant; apomixis;  
 KW plant breeding; seed production; SDS protein; cyclin box.  
 XX  
 XX Arabidopsis thaliana.  
 OS  
 OS WO200174144-A1.  
 PN  
 XX  
 XX PD 11-OCT-2001.  
 XX  
 XX PP 29-MAR-2001; 2001WO-US09875.  
 XX  
 XX PR 31-MAR-2000; 2000US-193523P.  
 XX  
 XX PA (UYPE-) UNIV PENNSYLVANIA STATE.  
 XX  
 XX  
 XX PI Ma H;  
 XX  
 XX DR WPI; 2001-662939/76.  
 XX  
 XX  
 XX PT A new plant gene from Arabidopsis, designated SDS, mutations in which  
 PT are associated with inability to produce pollen, is useful for the  
 PT production of male sterile plants for plant breeding -  
 XX  
 XX

Disclosure; Page 43; 47pp; English.

CC The patent discloses novel plant gene from Arabidopsis thaliana,  
 CC designated SDS, which is associated with a failure to maintain  
 CC homologue attachment during meiotic prophase I. The SDS gene is  
 CC located on chromosome 1 and is useful in plant breeding to produce  
 CC male sterile SDS mutants and cloned progeny by apomixis where  
 CC meiosis is bypassed in seed production. The gene may also be  
 CC used as a probe to identify related genes in other plant species,  
 CC and to identify and isolate other genes of the meiosis regulatory  
 CC pathway. The present sequence is Arabidopsis thaliana SDS protein  
 CC cyclin box.  
 CC  
 XX  
 XX

Sequence 145 AA:

Query Match 25.0%; Score 738; DB 22; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;  
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 MONTGLIRLRSIMVQWIVKQCSDMGLQOETFLFGVGLDRFLSKGSPKSERLLIVGLA 436  
 DB 1 mntglirrlrsimvwivkqcsdmglqgetlflgvglldrflskgsfkserllivgl 436  
 QY 437 SLTATRIENOPYNSIRKRNFTIONLRSRHEVVAEMVLVOEVLNKCFPTTFNPLMF 495  
 DB 61 sltatrieenopynsirkrnftionlrsrhevvaemvlvgevlnfkcfpttfnlwfv 120  
 QY 497 YLKAARNPEVERKAKSLAVTSLS 521  
 DB 121 ylkaarnpeverkakslavtslsd 145

RESULT 3

AAE35801 ID AAE35801 standard; Protein; 424 AA.

XX AC AAE35801;

XX DT 23-FEB-2001 (first entry)

DE Protein involved in cell cycle regulation seq ID 30.

XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;  
 KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;  
 XX cotton; rice; barley; millet.  
 XX  
 XX Zea mays.  
 OS



```

Db      96 slrsad-----kpsaklpappvargsaqlrhnnvppkptladvpsrapalvsc 148
QY      251 EKFSFEVNS-DLDESSBQNSLEYQYS-DPDYSDYTPSIFEDSGSESEKSSDSPISH 308
Db      149 glvpqrsqgdsv--ssdelmstcdsmkspdfeyvdnqdtsmias--lqrrtselhlrlise 203
QY      309 SRSLYQFEGFCRSTIPNDFGSSCEEINSELRFDDEEV-----EESYLRLRERER-- 361
Db      204 drveenkrlk--navapmeldrlc--dvds---yedpqlcatlasdlymlhlraeclck 256
QY      362 --SHAYMRDCAKATCSRMNDTGLIPRLRSIMVQIVKQCSDMQLQOETPLFVGLIDRFL 419
Db      257 rpsidlfmetlqk-----dvpsmtralllqlwlvveaceqylvdpctlylcvnyldryl 307
QY      420 SKGSFSESRITLIVGASLTLATRIEENQPYNSIRKRNET-IQNLRYSHREYVAMEMLYQ 478
Db      308 s-gneisrqrqlilgvcamliaakee---lcapqveefcytlndnytfidvldmeasvl 363
QY      479 EYLNFKCTPTITFNLFWYLKAAKANE-----VERKASLAVTSLSDOTQLCFMPSTIVA 533
Db      364 nylktemlapakcfltrfaraaqacdpalhlefianylaelilleyllsyppslia 423
QY      534 AALVYLA--CIEHNKISAYQFVIRKIVHRTDNEILPCVKSIL 572
Db      424 asaalfarflilqpkky-pwnstlahyqkykpsklasecvkal 463

```

## RESULT 5

AAB56707 standard; Protein: 515 AA.

AC AAB56707;

DT 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SEQ ID NO:1285.

Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioprotective; immunomodulatory; muscular; vulnereary; gastrotrophic; nephroprotective; antineoplastic; gynaecological; antibacterial; gene therapy; neutral; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.

OS Homo sapiens.

PN MO20005174-A1.

PD 21-SEP-2000.

PE 08-MAR-2000; 2000MO-US05988.

PR 12-MAR-1999; 9905-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM;

DR WPI: 2000-587513/55.

DR N-PSDB; AAR15910.

XX Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -

PS Claim 11; Page 1704-1706; 2338pp; English.

CC AAR15566 to AAR16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.

CC The prostate cancer antigens can have neuroprotective, cytostatic, cardioprotective, immunomodulatory, muscular, vulnereary, gastrointestinal.

CC nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAR15566 to AAR16514 to CC AAR57303 represent sequences used in the exemplification of the present invention.

XX Sequence 515 AA;

QY Query Match 7.1%; Score 208.5; DB 21; Length 515;

Best Local Similarity 24.6%; Pred. No. 4.8e-09;

Matches 88; Conservative 65; Mismatches 126; Indels 79; Gaps 13;

QY 214 EISKPSFVBAOSSIGSAKELPELEIVGCVSDLACSEK-----SEVSDSLD-D 263

Db 137 evrepa-----gssaqgqpkrrvaplklpvndehvtvppwkanakqpaftlhvd 187

QY 264 ESSEQRSEIYSQSPFDYSDYPSIFEDSG-----SEFSEKSSSDSPISHRS 311

Db 188 eaekkaqkpkpaesqkiered--alafnsalslpgqckplvpldypmdgfsesphmdms 244

QY 312 LVYQFQPCRSTIPNDFGSSCEEIHSELRFDDEEVESYLAIRERSHAYMRDCAK 371

Db 245 lyledekpyvsnvcpd-----yhedih-----lylremevk-----ckp 278

QY 372 AYCSRMNDTGLIPRLRSIMVQIVKQCSDMQLQOETPLFVGLIDRFLSKGSFSESRIT 431

Db 279 kvqymkqgpdltmsmralldvdlvegceyklqethlvanvndrlfslmsvllrgk-lq 337

QY 432 LVGIASLTLATRIEENQ-----YNSIRKRNETIQNLRYSHREYVAMEMLYQVNLNK 484

Db 338 lvglaamllaskfeelypveavefly-----ltdcytkkqvrlmehlvikvlltd 388

QY 485 CFPPTITFNLFWYLKAAKANEVERKASLAVTSLSD-QTQLCFMPSTVAAALVYLA 540

Db 389 laaptvngfltgylhqpnanckveslamflgelsltdadpylkylpvsiaagaftla 446

## RESULT 6

AAR13731 standard; Protein: 431 AA.

AC AAR13731;

DT 07-NOV-1991 (first entry)

DE Human cyclin A.

Human; cancer; Hepatitis B virus; cell proliferation; hepatitis; cirrhosis; hyperleucocytic acute myeloblastic leukaemia.

OS Homo sapiens.

PN MO9112324-A.

PD 22-AUG-1991.

PE 06-FEB-1991; 91WO-FR00089.

PR 12-FEB-1990; 90FR-0001596.

PA (INRM ) INSERM INST NAT SANTE.

PI Brechot C, Wang J, Henglein B, Zindy F;

DR WPI: 1991-267135/36.

DR N-PSDB; AAR13385.



PT New nucleotide sequence encoding human cyclin A - and derived  
 PT antibodies and anti-sense DNA, for diagnosis and treatment of  
 PT cell proliferation, respectively  
 XX  
 PS Disclosure: Page 15-16; 23pp; English.  
 CC  
 CC The human genome contains (on chromosome 4q27) a specific site for  
 CC integration of HBV into the cyclin A gene. Such integration  
 CC occurs in liver cells at early stages of tumour development without  
 CC significant chromosomal rearrangement or histological signs of  
 CC hepatitis or cirrhosis. Expression of cyclin A is associated with  
 CC cell deviation so integration of HBV interferes with regulation of  
 CC cell multiplication.  
 CC Antibodies to cyclin A are used to determine the cellular level of  
 CC cyclin A for diagnosis of cell proliferation. Compens. conty.  
 CC anti-sense cDNA can be used to treat such proliferation (by  
 CC blocking cyclin A expression). Partic., cyclin A is expressed  
 CC most highly in hyperleukocytic acute myeloblastic leukemia during  
 CC the period of rapid cell deviation and at very low level in primary  
 CC liver cancer when the rate of cell deviation is low.  
 CC  
 XX Sequence 431 AA;  
 SQ  
 Query Match 7.0%; Score 207; DB 12; Length 431;  
 Best Local Similarity 25.4%; Pred. No. 4.9e-09;  
 Matches 87; Conservative 60; Mismatches 126; Indels 70; Gaps 12;  
 QY 229 GSAKELPELEIVGCVSDLACSEK-----SEEVSDSLD-DESEGRSEITYQYSD 278  
 DB 59 glahqrkrttrvaplkdlpyndehvtpwkanakpafthvdeekagkpkpeasqk 118  
 QY 279 FVYSVTSPISFDSG-----SEFSEKSSSDSPISHRSYLQFEQFCRSTIP 326  
 DB 119 lered---alafnaslsipprkplvpdydmqsfesphumslvledekysvnevp 175  
 QY 327 NDFGSGCEEHISELLRDFDEBEVSEYRLRERRSHAYMRDCAKAYCSMDNTGLPRL 386  
 DB 176 d-----yhedih-----tylremevk-----ckrkvgymkkpddltm 209  
 QY 387 RSIMVOMIVKCCSDMGLQOETFLGGLDRFLSKSGFSKSPRTILVGCISLTLATRIE 446  
 DB 210 rdlldwlvvegeeyklqnehlavnyidflfssmsvlgk-lqlvgtaamlakfee 268  
 QY 447 NOP-----YNSIKRNFNTIONLRYSREHVAEMELVOEYLNKCTPTIPNPL-WFVL 498  
 DB 269 lyppevaeefvy-----ltdcltylkkqylrmehlvlyvltfdlaapvngflqyfl 319  
 QY 499 KAARANPEVERAKSLAVTSLD-OTOLCEFWSTVAALVYIA 540  
 DB 320 hqgpmckvesiamflgelsliddpylkylpvsiaaafnla 362  
 RESULT 7  
 AAB35799 standard; Protein: 449 AA.  
 ID AAB35799 standard; Protein: 449 AA.  
 XX  
 AC AAB35799;  
 XX  
 DT 23-FEB-2001 (first entry)  
 DE Protein involved in cell cycle regulation SEQ ID 22.  
 XX  
 XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;  
 KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;  
 KM cotton; rice; barley; millet.  
 XX  
 OS Zea mays.  
 XX  
 PN WO2000065040-A2.  
 XX  
 PD 02-NOV-2000.

PF 13-APR-2000; 2000MO-US09975.  
 XX  
 PR 22-APR-1999; 99US-0130849.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Helent[aris TG, Habben JE, Sun Y;  
 XX  
 DR WPI: 2000-687333/67.  
 DR N-PSDB: AAC83106.  
 XX  
 XX Nucleic acids useful for producing transgenic plants, preferably maize,  
 PT and/or cyclin-dependent kinase -  
 CC  
 PS Claim 16; Page 99-100; 122pp; English.  
 CC  
 CC polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -  
 CC AAB35806 which are involved in regulating the cell cycle. The protein and  
 CC DNA sequences have been isolated from Zea mays (corn), and the invention  
 CC also includes oligonucleotides AAC83114 - AAC83139 which are related to  
 CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences  
 CC are useful for producing transgenic plants such as maize, soybean,  
 CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and  
 CC millet with increased levels of cell cycle gene activity, such as  
 CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are  
 CC also useful as probes for detecting deficiencies in the level of mRNA in  
 CC screening for desired transgenic plants, for detecting mutations in the  
 CC gene, for monitoring upregulation of expression or changes in enzyme  
 CC activity in screening assays of compounds, for detecting any number of  
 CC allelic variants, orthologs or paralogs of the gene, and site-directed  
 CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for  
 CC recombinant expression of the encoded polypeptides and as immunogens for  
 CC preparing and screening antibodies. A transgenic plant comprising an  
 CC expression cassette including a cell cycle regulatory gene is useful for  
 CC assaying enzyme agonists and antagonists, and as immunogens or antigens  
 CC to obtain antibodies. The antibodies are useful in assaying expression  
 CC levels of cell cycle regulatory proteins, for identifying and isolating  
 CC nucleic acids from expression libraries, for identifying homologues of  
 CC polypeptides from other species, and for purification of the proteins.  
 CC  
 XX Sequence 449 AA;  
 SQ  
 Query Match 6.7%; Score 198.5; DB 21; Length 449;  
 Best Local Similarity 23.4%; Pred. No. 2.8e-08;  
 Matches 83; Conservative 70; Mismatches 136; Indels 65; Gaps 13;  
 QY 231 AKELPELEIVGCVSDLACSEKSEEVSDSLDDESEGRSEITYQYSDPDYADYPSIF 290  
 DB 110 akpppe-dvlyvlsd-----segatqlaessasvtr-----kxin 147  
 QY 291 DSGSEFSEKSSSDSPISHRSYLQFEQFCRSTIPNDFGSGCEEHISELLRDFDEVE 350  
 DB 148 tlvslsarskaacgltcktr-----gvaviedad---klvnnelavveyledi 194  
 QY 351 ESYRLRERERSHAYMRDCAKAYCSMD-NTGLIPRLRSIMVOMIVKCCSDMGLQOETFL 409  
 DB 195 ytfykiaqhndrip-----cdyldtqvelnprmlrlagvlienhkkelmpely 244  
 QY 410 LGVGLDRFLSKSGFSKSEKRLILVGISLTLATRIE--NQPYNSIKRNFNTIONLRYSR 467  
 DB 245 ltmylidqylslgpr-lrrelqlvgvsamllackyeelwapevndf---llsdsaysr 299  
 QY 468 HEVVAEMELVOEYLNKCTPTIPNPLFWFLKAAARNPVERAKS-----LAVTSL 520  
 DB 300 eqllismekglnslenmltvpvymflvfrllkaaalgnhvkemennwfffealalmgy 359  
 QY 521 DGTQLCTPSTVAALVYLACIEHNKISAYORYIKVH--RTTNDELPECVKS 572  
 DB 360 lvtlrl--pslvaasvyaarlcltkraplwtclkhghyffresetellectkl 410

RESULT 8  
 ID AAB43702 standard; Protein: 420 AA.  
 AC AAB43702;  
 DT 08-FEB-2001 (first entry)  
 DE Human cancer associated protein sequence SEQ ID NO:1147.  
 KM Human: cancer associated gene; cancer antigen; detection; cancer;  
 KM diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
 KM antidiabetic; antistatic; antirheumatic; antiarthritic; antiviral;  
 KM antineoplastic; antihypertensive; antiallergic; antibacterial; cardiant;  
 KM dermatological; neuroprotective; thrombolytic; coagulant; neotropic;  
 KM vasotropic; antipruritic; antineoplastic; gene therapy; inflammation;  
 KM immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KM allergic reaction; graft versus host disease; organ rejection;  
 KM haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KM neurological disease; drug screening.  
 OS Homo sapiens.  
 PN MO20055350-A1.  
 PD 21-SEP-2000.  
 XX 08-MAR-2000; 2000MO-US05682.  
 XX 12-MAR-1999; 9905-0124270.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM;  
 XX WPI: 2000-587533/55.  
 XX N-PSDB: AAC77911.  
 DR Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer -  
 XX Claim 11; Page 1763-1764; 2352pp; English.  
 PS AAC77607 to AAC78448 encode the human cancer associated proteins given  
 CC in AAB43398 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnery; immunomodulator;  
 CC antidiabetic; antistatic; antirheumatic; antiarthritic;  
 CC antineoplastic; antihypertensive; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC neotropic; vasotropic; antipruritic; antineoplastic; gene therapy;  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention.  
 XX Sequence 420 AA;  
 SQ

Query Match 5.68; Score 196; DB 21; Length 420;  
 Best Local Similarity 31.78; Pred. No. 4.1e-08;  
 Matches 63; Conservative 38; Mismatches 88; Indels 10; Gaps 5;  
 377 MDNGLIPRLSIWQWIVKQSDMGLQDTEFLVGLDRLFSKSFSEKTLIVGIA 436

Db 178 lqgrdingrmraillvqmwvqnskfxllqetlqmcvglmeflqvgrv-srkklqvgile 236  
 QY 437 SLTLATRIEENOPYSIRKRNPT-IQNLRYSRHEVVAWMLVDELFNKCFPTIRNFJM 495  
 Db 237 allaskyemefspol---edfvyldnaysqirremetlilkelxfelgrplphlfr 293  
 QY 496 FYLKARANDPEVERKAKSLAVTSISDQTOCLFNPSTVAALVYLACIEHMKISANYRVIX 555  
 Db 294 raskagevdvqhlakylmetlildymvnyhpskvaad---ascisqkvlgqkwnlk 350  
 QY 556 VHVRT--TUNELPECVKSL 572  
 Db 351 qgylylgvlenevlvwmqjm 369  
 RESULT 9  
 ID AAM87566 standard; Protein: 398 AA.  
 AC AAM87566;  
 DT 05-MAR-1999 (first entry)  
 DE A cyclin related protein HCRP-2.  
 KM Human cyclin related protein; HCRP; HCRP-2; cancer; adenocarcinoma;  
 KM leukaemia; immune disorder; AIDS; asthma; developmental disorder;  
 KM renal tubular acidosis; cerebral palsy.  
 OS Homo sapiens.  
 PN MO985510-A2.  
 PD 10-DEC-1998.  
 XX 05-JUN-1998; 98MO-US11735.  
 XX 05-JUN-1997; 97US-0870143.  
 XX (INCY-) INCYTE PHARM INC.  
 XX Cocks BG, Corley NC, Guegler KJ, Hillman JL, Shah P;  
 XX WPI: 1999-045731/04.  
 XX N-PSDB: AAV83711.  
 DR Human cyclin related protein, HCRP - useful, e.g. to diagnose and  
 PT treat cancer, immune disorders and developmental disorders and  
 PT screen for antagonists used to treat cancer  
 XX Claim 19; Fig 2A-F; 80pp; English.  
 PS The present sequence represents a human cyclin related protein (HCRP)  
 CC designated HCRP-2 HCRP proteins can be used to treat cancer e.g.  
 CC adenocarcinoma, leukaemia, etc. or immune disorders e.g. AIDS,  
 CC asthma. They can also be used to treat developmental disorders,  
 CC e.g. renal tubular acidosis, cerebral palsy. HCRP-2 was expressed in  
 CC cancers and foetal tissues, and increased expression was proposed to  
 CC be associated with cancer and decreased expression with developmental  
 CC disorders. HCRP can be used to screen for agonists (useful to treat  
 CC conditions as above) or antagonists. It can be used to generate  
 CC antibodies, useful as antagonists or to diagnose conditions characterised  
 CC by HCRP expression and to monitor therapeutic interventions.  
 CC Polynucleotides encoding HCRP can be used to detect polynucleotides  
 CC encoding HCRP, e.g. to diagnose diseases relating to polynucleotide  
 CC expression or monitor HCRP regulation during therapeutic intervention.  
 CC They are useful to produce complementary or antisense sequences for  
 CC therapeutic administration to modulate or prevent HCRP expression e.g. to  
 CC treat or prevent cancers as above.  
 XX Sequence 398 AA;  
 SQ



CC of a contig composed of clones isolated from corn endosperm  
CC and mesocotyl cDNA libraries. It represents 80% of the protein  
CC (the C-terminal region). The invention relates to isolated nucleic  
CC acid fragments (see A421993-66) encoding cyclin A, cyclin delta-1,  
CC cyclin delta-2 and cyclin delta-3 polypeptides (see A471889-902).  
CC It also relates to the construction of chimeric genes encoding all  
CC or a portion of a cyclin, in sense or antisense orientation, where  
CC expression of the chimeric gene results in altered levels of the  
CC cyclin protein in a transformed host cell. This would have the  
CC effect of altering the regulation of cell division in those cells.  
CC The nucleic acid fragments may be used to express cyclins in plant  
CC cells to enhance cell tissue culture growth. The availability of  
CC nucleic acid sequences encoding all or a portion of cyclins should  
CC facilitate studies of cell cycle in plants, provide genetic tools  
CC to enhance cell growth in tissue culture, increase the efficiency  
CC of gene transfer and help provide more stable transformations. The  
CC proteins can be used as targets to facilitate design and/or  
CC identification of inhibitors of those enzymes that may be useful as  
CC herbicides.

XX Sequence 295 AA;

Query Match 6.6%; Score 194; DB 20; Length 295;

Best Local Similarity 28.2%; Pred. No. 3.5e-08;

Matches 67; Conservative 51; Mismatches 84; Indels 36; Gaps 9;

QY 352 SYLRLRESHAMVRDCAKAYCSRMDNTGLIPRLSITMOWIVKQCSMDGQDQTLPLG 411

Db 31 LYLRLSVDPQRRSRSSYLEAV-----GADVTAHMSLLVDVLAEEYKLVADLLYL 85

QY 412 VGLDRFLSKGSEKSEKTLILVGIASULTATRIENOPNYSIRKNFT-IONLRYSRHEV 470

Db 86 ISYDRTLSVNAIGRDK-IQLLYVASMLIAAKFEELSPH---PDFCYLDNCTYKEEL 141

QY 471 VAMMLVOEVLNFCPTPTFENFLWYTKAARANPE-----VERAKSLAATYSDDQQL 525

Db 142 IKMESDILKILKELGMPKTKTLIRTSANEKKGSLIMEFLGYSYLAELSIDGYCL 201

QY 526 CFMPSTVAALVLA--CIEHN-----KISAYORVKKVHRTDNELEPECVKSL 572

Db 202 RFLPSVVAASVMFVARPDIDPNTCPWTKLQKMTGY---KV-----SELKDLVAL 249

RESULT 12

AG24671 standard; Protein; 348 AA.

AC AG24671;

DT 17-OCV-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28436.

KM Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.

OS Arabidopsis thaliana.

PN EPI033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 26-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134370.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
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PR 16-JUN-1999; 99US-0139452.  
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PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139889.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140655.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142380.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.

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PR	13-OCT-1999	9905-01559294
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PR	26-OCT-1999	9905-01613559
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PR	26-OCT-1999	9905-01613561
PR	26-OCT-1999	9905-01619920
PR	26-OCT-1999	9905-01619921
PR	28-OCT-1999	9905-01619943
PR	28-OCT-1999	9905-01621442

Query Match 6.5%; Score 193; DB 21; Length 348;  
 Best Local Similarity 27.1%; Pred. No. 5.6e-08;  
 Matches 61; Conservative 57; Mismatches 91; Indels 16; Gaps 71

[illegible]

RESULT	13
AA024670	
ID	AA024670 standard; Protein; 360 AA.
XX	
AC	AA024670;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 28435.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
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PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
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PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
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PR 22-JUN-1999; 99US-0139899.  
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PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 28-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
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PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
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PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
  
PR 15-JUL-1999; 99US-0144005.  
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PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
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PR 26-JUL-1999; 99US-0145276.  
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PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147312.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
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PR 27-AUG-1999; 99US-0151085.  
PR 27-AUG-1999; 99US-0151086.  
PR 27-AUG-1999; 99US-0151086.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151338.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
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PR 15-SEP-1999; 99US-0154018.  
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PR 05-OCT-1999; 99US-0157753.

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PR 25-OCT-1999; 99US-0161404.  
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PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161320.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 6.5%; Score 193; DB 21; Length 360;  
Best Local Similarity 27.1%; Pred. No. 5 9e-08;  
Matches 61; Conservative 57; Mismatches 91; Indels 16; Gaps 7;

OY 352 SYLRERERSHAWRDCAACVCSRDNGILRLRSINWQIVKQCSDMGLQOETFLG 411  
DB 92 aylremegkphrpdp---ylekv qsdltphmraivdwiveaeeykivsdltlylt 146  
OY 412 VGLDRFLSKFSKFSKFTLIVGLASLTATRIEENQPNYSIKRNF--IONLRYSPHEV 470  
DB 147 lsydrflsvpnrqr-ldlvgsamllaskyeelgp---pkvedfcyidntltkgev 202  
OY 471 VAMEMLVQEVLENKCFPTPTFNFLMEFLYKAAR---ANPEVERKAKSLAVTSLSDQTL 525  
DB 203 vsmeadl1la1qfeligspitktflrfttrvagedfkdsqqlieflccylselsmdlytcv 262  
OY 526 CFMPSTVAALVLA-CIEHNKISAVQRIKIVHPTDNDLEPCV 569  
DB 263 kypslslsasvfiarflirpqbpmgmleeytkykaadlygc 307

RESULT 14  
AAG24669  
ID AAG24669 standard; Protein; 369 AA.  
AC AAG24669;  
XX 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 28434.  
DE Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX Arabidopsis thaliana.  
OS EPI033405-A2.  
PM EPI033405-A2.  
XX 06-SEP-2000.  
PD

XX 25-FEB-2000; 2000EP-0301439.  
PF 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 16-APR-1999; 99US-0128714.  
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PR 21-APR-1999; 99US-0130077.  
PR 23-APR-1999; 99US-0130449.  
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PR 04-MAY-1999; 99US-0132407.  
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PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 25-MAY-1999; 99US-0135629.  
PR 27-MAY-1999; 99US-0136021.  
PR 28-MAY-1999; 99US-0136392.  
PR 01-JUN-1999; 99US-0136782.  
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PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138099.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
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PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
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PR 18-JUN-1999; 99US-0139730.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.







